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(54) **Recombinant transglutaminase**
Rekombinante Transglutaminase
Transglutaminase recombinante

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Description**FIELD OF THE INVENTION**

5 This invention relates to a DNA gene which encodes transglutaminase, a plasmid in which the gene is incorporated, a transformant transformed with the plasmid and a process for the production of transglutaminase which comprises culturing the transformant.

BACKGROUND OF THE INVENTION

10 Transglutaminase (hereinafter, referred to as "BTG") is an enzyme which catalyzes an acyl transfer reaction of a γ -carboxyamide group of glutamine residue in a peptide chain.

BTG induces intramolecular or intermolecular formation of ϵ -(γ -Gln)-Lys cross linking when an ϵ -amino group of a lysine residue in a protein molecule functions as an acyl receptor. Also, when water functions as an acyl receptor, this enzyme accelerates conversion of glutamine residues into glutamic acid residues by deamidation.

15 Because of its function to gel protein, BTG has been employed in the production of gelled food, gelled cosmetics, yogurt, gelatins, cheese and the like (JP-B-1-50382). (The term "JP-B" as used herein means an "examined Japanese patent publication".) This enzyme has also been employed in the production of thermally stable materials such as microcapsules, carriers of immobilized enzymes and the like.

20 BTG has been found in animals, for example, in the liver of guinea pigs (Connellan et al., Journal of Biological Chemistry, vol. 246, No. 4, pp. 1093-1098 (1971)) and in various organs and blood of mammals (Folk et al., Advances in Enzymology, vol. 38, pp. 109-191 (1973); and Folk et al., Advances in Protein Chemistry, vol. 31, pp. 1-133 (1977)), and its enzymological properties have been studied. In addition, a different type of BTG, which is independent of calcium (Ca^{2+}) and is therefore different from the animal-derived BTG, has been found in various strains of the genus Streptovorticillium. Illustrative examples of these strains include Streptovorticillium griseocarneum IFO 12776, Streptovorticillium cinnamoneum sub sp. cinnamoneum IFO 12852, Streptovorticillium mobaraense IFO 13819 and other species (cf. JP-A-64-27471). (The term "JP-A" as used herein means an "unexamined published Japanese patent application".)

25 Since BTG is obtained from animals, microorganisms and the like, there are many problems to be solved such as a low production yield and an expensive production cost.

30 As a result of extensive investigations to overcome these problems of the prior art, the inventors of the present invention have succeeded in isolating and purifying a DNA gene which encodes BTG and determining its base sequence. On the basis of these results, the present inventors have provided a method for producing BTG efficiently in a large quantity through expression of the DNA gene in microorganisms such as Escherichia coli using genetic engineering.

SUMMARY OF THE INVENTION

35 In view of the above, it therefore is a primary object of the present invention to provide a DNA fragment which encodes transglutaminase, a plasmid in which the DNA fragment is incorporated, a transformant transformed with the plasmid and a process for the production of transglutaminase that comprises culturing the transformant.

40 These and other objects and advantages of the present invention will become apparent from the following description.

BRIEF DESCRIPTION OF THE ACCOMPANYING DRAWING

45 The drawing shows the results of Western blotting obtained in Example 4 hereinafter.

DETAILED DESCRIPTION OF THE INVENTION

50 In accordance with the present invention, there is provided a DNA fragment which encodes BTG, more particularly, a DNA fragment containing a base sequence that encodes an amino acid sequence as shown in the Table 1 below wherein each amino acid is indicated by the corresponding single letter code.

TABLE 1

5	10 DSDDRVTTPA	20 EPLDRMPDPY	30 RPSYGRAETV	40 VNNYIRKWQQ
	50 VYSHRDGRKQ	60 QMTEEQREWL	70 SYGCVGVTV	80 NSGQYPTNRL
10	90 AFASFDEDRF	100 KNELKNGRPR	110 SGETRAEFEG	120 RVAKESFDEE
	130 KGFQRAREVA	140 SVMNRALENA	150 HDESAYLDNL	160 KKELANGNDA
15	170 LRNEDARSPF	180 YSALRNTPSF	190 KERNGGNHDP	200 SRMKAVIYSK
	210 HFWSGQDRSS	220 SADKRKYGDP	230 DAFRPAPGTG	240 LVDMSRDRNI
20	250 PRSPTSPGEG	260 FVNFDYGWFG	270 AQTEADADKT	280 VWTHGNHYHA
25	290 PNGSLGAMHV	300 YESKFRNWSE	310 GYSDFDRGAY	320 VITFIPKSWN
	330 TAPDKVKQGW	P		

(SEQ ID NO: 1)

This DNA fragment can include various alternative base sequences when codon degeneracy is taken into consideration and these are within the scope of the present invention. It is apparent that these base sequences can be selected easily by those skilled in the art based on many factors related to the genetic expression system such as host cell-dependent preferential codons and the like.

As an illustrative example of such a case, a base sequence which can be used suitably in an expression system using E. coli or yeast as the host cell is shown in Table 2 below.

TABLE 2

5	GAT	TCT	GAT	GAC	AGA	GTC	ACT	CCA	CCA	GCT
	GAA	CCA	TTG	GAT	AGA	ATG	CCA	GAT	CCA	TAC
	AGA	CCA	TCT	TAC	GGT	AGA	GCT	GAA	ACT	GTT
10	GTC	AAC	AAC	TAC	ATT	AGA	AAG	TGG	CAA	CAA
	GTC	TAC	TCT	CAC	AGA	GAT	GGT	AGA	AAG	CAA
15	CAA	ATG	ACT	GAA	GAA	CAA	AGA	GAA	TGG	TTG
	TCT	TAC	GGT	TGT	GTT	GGT	GTT	ACT	TGG	GTT
	AAC	TCT	GGT	CAA	TAC	CCA	ACT	AAC	AGA	TTG
20	GCT	TTC	GCT	TCT	TTC	GAT	GAA	GAT	AGA	TTC
	AAG	AAC	GAA	TTG	AAG	AAC	GGT	AGA	CCA	AGA
25	TCC	GGT	GAA	ACT	AGA	GCT	GAA	TTC	GAA	GGT
	AGA	GTT	GCT	AAG	GAA	TCT	TTC	GAT	GAA	GAA
30	AAG	GGT	TTC	CAA	AGA	GCT	AGA	GAA	GTT	GCT
	TCT	GTT	ATG	AAC	AGA	GCT	CTA	GAA	AAC	GCT

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	CAC	GAT	GAA	TCT	GCT	TAC	TTG	GAT	AAC	TTG
5	AAG	AAG	GAA	TTG	GCC	AAC	GGT	AAC	GAT	GCT
	TTG	AGA	AAC	GAA	GAT	GCT	AGA	TCC	CCA	TTC
10	TAC	TCT	GCT	TTG	AGA	AAC	ACT	CCA	TCT	TTC
	AAG	GAA	AGA	AAC	GGT	GGT	AAC	CAC	GAT	CCA
	TCC	AGA	ATG	AAG	GCT	GTT	ATT	TAC	TCT	AAG
15	CAC	TTC	TGG	TCT	GGT	CAA	GAT	AGA	TCT	TCT
	TCT	GCT	GAT	AAG	AGA	AAG	TAC	GGT	GAT	CCA
20	GAT	GCT	TTC	AGA	CCA	GCT	CCA	GGT	ACC	GGT
	TTG	GTC	GAC	ATG	TCC	AGA	GAT	AGA	AAC	ATT
	CCA	AGA	TCC	CCA	ACT	TCT	CCA	GGT	GAA	GGT
25	TTC	GTC	AAC	TTC	GAT	TAC	GGT	TGG	TTC	GGT
	GCT	CAA	ACT	GAA	GCT	GAT	GCT	GAT	AAG	ACT
30	GTT	TGG	ACC	CAT	GGT	AAC	CAC	TAC	CAC	GCT
	CCA	AAC	GGT	TCT	TTG	GGT	GCT	ATG	CAC	GTC
35	TAC	GAA	TCT	AAG	TTC	AGA	AAC	TGG	TCT	GAA
	GGT	TAC	TCT	GAT	TTC	GAT	AGA	GGT	GCT	TAC
	GTT	ATT	ACT	TTC	ATT	CCA	AAG	TCT	TGG	AAC
40	ACT	GCT	CCA	GAC	AAG	GTC	AAG	CAA	GGT	TGG
	CCA									

(SEQ ID NO: 2)

The DNA fragment shown in Table 1 above can be easily prepared by prior art techniques such as chemical synthesis and the like, for example, the phosphormidite method (M.H. Caruthers, Science, 230, 281 (1985) and Sinha, N.D. et al., Nucleic Acids Res., 12, 4539-4557 (1984).

A further illustrative example of a DNA fragment containing a base sequence coding for the amino acid sequence shown in Table 1 is the structural gene of BTG corresponding to the amino acid sequence shown in Table 1, which is shown in Table 3 below.

TABLE 3

5 GACTCCGACGACAGGGTCACCCCTCCCGCCGAGCCGCTCGACAGGATGCCCCGACCC
 GTACCGTCCCTCGTACGGCAGGGCCGAGACGGTCGTCAACAACCTACATACGCAAGT
 GGCAGCAGGTCTACAGCCACCGCGACGGCAGGAAGCAGCAGATGACCGAGGAGCAA
 10 CGGGAGTGGCTGTCTACGGCTGCGTCGGTGTACCTGGGTCAATTCGGGTCTAGTA
 CCCCACGAACAGACTGGCCTTCGCGTCTTCGACGAGGACAGGTTCAAGAACGAGC
 15 TGAAGAACGGCAGGCCCCGGTCCGGCGAGACGCGGGCGGAGTTCGAGGGCCGCGTC
 GCGAAGGAGAGCTTTGATGAAGAGAAGGGGTTCAGCGGGCGCGTGAGGTGGCGTC
 CGTGATGAACAGGGCCCTGGAGAACGCCCACGACGAGAGCGCTTACCTCGACAACC
 20 TCAAGAAGGAACTGGCGAACGGCAACGACGCCCTGCGCAACGAGGACGCCCCGTTCC
 CCGTTCTACTCGGCGCTGCGGAACACGCCGTCCTTTAAGGAGCGGAACGGAGGCAA
 25 TCACGACCCGTCCAGGATGAAGGCCGTCATCTACTCGAAGCACTTCTGGAGCGGCC
 AGGACCGGTTCGAGTTCGGCCGACAAGAGGAAGTACGGCGACCCGGACGCTTTCGCG
 30 CCGGCCCCCGGGACCGGCCTGGTCGACATGTTCGAGGGACAGGAACATTCCGCGCAG
 CCCCACCAGCCCCGGTGAGGGATTTCGTCAATTTCTGACTACGGCTGGTTTCGGCGCCC
 AGACGGAAGCGGACGCCGACAAGACCGTCTGGACCCACGGAAATCACTATCACGCG
 35 CCCAATGGCAGCCTTGGTGCCATGCATGTATACGAGAGCAAGTTCGCGAACTGGTC
 CGAAGGTTACTCCGACTTCGACCGCGGAGCCTATGTGATCACCTTCATCCCCAAGA
 40 GCTGGAACACCGCCCCGACAAGGTAAAGCAGGGCTGGCCG

(SEQ ID NO: 3)

45 The DNA fragment according to the present invention is not particularly limited to the DNA fragment containing a base sequence that encodes the amino acid sequence shown in Table 1. The encoded amino acid sequence may be different from the sequence shown in Table 1 in that a part of the sequence thereof is missing or replaced with some other amino acid sequence and/or in that some other amino acid sequence is added to or inserted in the sequence, provided that a protein having such an amino acid sequence has transglutaminase activity or can be processed to become a mature protein which has transglutaminase activity. Thus, a DNA fragment containing a base sequence coding for such a different amino acid sequence is also included within the scope of the present invention.

50 The present invention also provides a DNA fragment containing a base sequence coding for an amino acid sequence in which 5' end of the DNA sequence encoding the amino acid sequence of Table 1 is further connected with a DNA fragment encoding all or part of the amino acid sequence containing a signal peptide as shown in Table 4 below.

TABLE 4

-75 -70 -60 -50
 MRYTP EALVFATMSA VYAPPDSCRR PARPPPTMAR

 -40 -30 -20 -10
 GKRRSPTPKP TASRRMTSRH QRAQRSAPAA SSAGPSFRAP

(SEQ ID NO: 4)

An example of the part of the amino acid sequence shown in Table 4 is shown in Table 5 below.

TABLE 5

-39 -30 -20 -10
 KRRSPTPKP TASRRMTSRH QRAQRSAPAA SSAGPSFRAP

(SEQ ID NO: 5)

The above-described DNA fragments can also include various base sequences based on codon degeneracy, and they can be prepared by various well known techniques including chemical synthesis.

An example of a base sequence of a DNA fragment encoding the amino acid sequence containing a signal peptide as shown in Table 4 is shown in Table 6 below.

TABLE 6

ATGCGCTATACGCCGAGGCTCTCGTCTTCGCCACTATGAGTGCGGTTTATGCACC
 GCCGGATTTCATGCCGTCGGCCGGCGAGGCCGCCGCCGACAATGGCGCGGGGAAGA
 GACGAAGTCCTACGCCGAAACCTACCGCCTCACGGCGGATGACGTCGCGACATCAA
 CGCGCTCAACGAAGCGCTCCGGCCGCTTCGAGCGCCGGCCCGTCGTTCCGGGCCCC
 C

(SEQ ID NO: 6)

An example of a base sequence of a DNA fragment encoding the amino acid sequence as shown in Table 5 is shown in Table 7 below.

TABLE 7

AAGAGAAGATCTCCTCAACTCCAAAGCCAACTGCTTCTAGAAGAATGACTTCTAGACA
 CCAAAGAGCTCAAAGATCTGCTCCAGCTGCTTCTTCTGCTGGTCCATCTTTCAGAG
 CTCCA

(SEQ ID NO: 7)

The DNA fragment according to the present invention can be also produced by cloning it from genomic DNA library

of actinomycetes using a DNA fragment as a probe prepared using polymerase chain reaction (PCR) technology (R.F. Saiki et al., *Science*, 239, 487 (1988) and K.B. Mullis and F.A. Faloona, *Methods Enzymol.*, 155, 335 (1989)). An example of a base sequence of a DNA fragment obtained in this manner which contains all of the above-described DNA fragment, i.e., the structural gene of BTG and an upstream portion from its 5' end is shown in Table 8 below.

TABLE 8

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10  ATGCGCTATACGCCGAGGCTCTCGTCTTCGCCACTATGAGTGCGGTTTATGCACC
    GCCGGATTTCATGCCGTCGGCCGGCGAGGCCGCCGCCGACAATGGCGCGGGGAAGA
    GACGAAGTCCTACGCCGAAACCTACCGCCTCACGGCGGATGACGTCGCGACATCAA
15  CGCGCTCAACGAAGCGCTCCGGCCGCTTCGAGCGCCGGCCCGTCGTTCCGGGGCCCC
    CGACTCCGACGACAGGGTCACCCCTCCCGCCGAGCCGCTCGACAGGATGCCCCGACC
    CGTACCGTCCCTCGTACGGCAGGGCCGAGACGGTCGTCAACAACCTACATACGCAAG
20  TGGCAGCAGGTCTACAGCCACCGCGACGGCAGGAAGCAGCAGATGACCGAGGAGCA
    ACGGGAGTGGCTGTCTTACGGCTGCGTCGGTGTCACCTGGGTCAATTCGGGTCAGT
    ACCCCACGAACAGACTGGCCTTCGCGTCCTTCGACGAGGACAGGTTCAAGAACGAG
    CTGAAGAACGGCAGGCCCGGTCCGGCGAGACGCGGGCGGAGTTCGAGGGCCGCGT
30  CGCGAAGGAGAGCTTTGATGAAGAGAAGGGGTTCAGCGGGCGCGTGAGGTGGCGT
    CCGTGATGAACAGGGCCCTGGAGAACGCCACGACGAGAGCGCTTACCTCGACAAC
    CTCAAGAAGGAACTGGCGAACGGCAACGACGCCCTGCGCAACGAGGACGCCCCGTTC
    CCCGTTCTACTCGGCGCTGCGGAACACGCCGTCTTTAAGGAGCGGAACGGAGGCA
40  ATCACGACCCGTCCAGGATGAAGGCCGTCTACTCGAAGCACTTCTGGAGCGGC
    CAGGACCGGTCGAGTTCGGCCGACAAGAGGAAGTACGGCGACCCGGACGCTTTCCG
    CCCGGCCCCCGGGACCGGCTGGTTCGACATGTCGAGGGACAGGAACATTCCGCGCA
    GCCCCACCAGCCCCGGTGAGGGATTCGTCAATTTGACTACGGCTGGTTCCGGCGCC
45  CAGACGGAAGCGGACGCCGACAAGACCGTCTGGACCCACGGAAATCACTATCACGC
    GCCCAATGGCAGCCTTGGTGCCATGCATGTATACGAGAGCAAGTTCCGCAACTGGT
    CCGAAGGTACTCCGACTTCGACCGCGGAGCCTATGTGATCACCTTCATCCCCAAG
    AGCTGGAACACCGCCCCCGACAAGGTAAAGCAGGGCTGGCCG
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(SEQ ID NO: 8)

According to the present invention, there is also provided a vector which can be used for expression and secretion

of BTG.

Such a vector may be prepared using conventional techniques by inserting a DNA fragment containing a base sequence which encodes the amino acid sequence shown in Table 1 into a known expression vector which is selected depending on the expression system desired. For example, when an *E. coli* strain is used as the host cell, commonly used vectors such as pTrc99A (Pharmacia); pPROK-C and pKK233-2 (Clontech Co.); and pNH8a, pNH16a, pNH18a, pcDNAII, and pAX (Stratagene) can be used for the construction of an expression secretion vector of the present invention. In addition, a plasmid pIN-III-ompA2 can be also used preferably. A plasmid, designated herein pOMPA-BTG, is an illustrative example of the expression secretion plasmid of the present invention which has been constructed by inserting the DNA fragment of the present invention into pIN-III-ompA2.

When an actinomycetes strain is used as the host cell, commonly used vectors such as pIJ 41, pSEV 2, pOA 154 and pSCP 111, etc. can be also used. In addition, pIJ 702 can be also used preferably. Further, when a yeast strain is used as the host cell, commonly used vectors such as pAM82, pYG100, YEp52, pAAH5, YCpADI, pYαEGF-23, YEpPT-ISIFN-α2, CPOTinsulin and pcD-Y (cf. Jikkenigaku, vol. 5, No. 11, 138 (1987)), etc. can be used. In addition, an *E. Coli*-yeast shuttle vector pNJ 1053 can be also used preferably. Illustrative examples of the expression secretion vector of the present invention which has been constructed by inserting the DNA fragment of the present invention into these vectors are pIJ702-BTG, pNJ1053-proBTG, and pNJ1053-BTG.

The present invention also relates to various transformants obtained by transforming host cells with the BTG gene-carrying expression and secretion vector.

Host cells suitable for use in such transformation purpose may be selected from various procaryotic cells and eucaryotic cells. As the procaryotic host, *E. coli* strains, *Bacillus* strains such as *B. subtilis*, actinomycetes (particularly, *Streptomyces* strains such as *Streptomyces lividans*, *Streptomyces coelicolor*, *Streptomyces kasugaensis*, and *Streptomyces parvulus*), and the like may be mentioned. As the eucaryotic host, yeasts (particularly, *Saccharomyces* strains such as *Saccharomyces cerevisiae*), other fungi such as *Aspergillus* strains etc., and the like may be mentioned.

An illustrative example of a useful *E. coli* strain is JA 221 strain (hsdM⁺, trpE5, leuB6, lacY, recA/F', lacI^q, lac⁺, pro⁺). A transformant was obtained by transforming *E. coli* JA 221 strain with the inventive expression and secretion plasmid pOMPA-BTG. This transformant, designated AJ12569 herein, was deposited by the present inventors on September 28, 1990, with Fermentation Research Institute, Agency of Industrial Science and Technology under the deposit number FERM P-11745 (FERM BP-3558 under the Budapest Treaty).

An illustrative example of a useful actinomycetes strain is *Streptomyces lividans* 3131-TS which was isolated from *Streptomyces lividans* 3131 as an thiostrepton-sensitive strain. A transformant which was obtained by transforming *Streptomyces lividans* 3131-TS with the inventive expression and secretion vector pIJ702-BTG, designated *Streptomyces lividans* AKW-1, was deposited by the present inventors on September 30, 1991, with Fermentation Research Institute, Agency of Industrial Science and Technology under the deposit number FERM BP-3586 under the Budapest Treaty.

An illustrative example of a useful yeast strain is *Saccharomyces cerevisiae* KSC22-IC (MATa, ss1 1, leu 2, his⁻, ura 3). A transformant which was obtained by transforming *Saccharomyces cerevisiae* KSC22-IC with the inventive expression and secretion vector pNJ1053-proBTG, designated *Saccharomyces cerevisiae* AJ 14669, was deposited by the present inventors on September 30, 1991, with Fermentation Research Institute, Agency of Industrial Science and Technology under the deposit number FERM BP-3585 under the Budapest Treaty.

The present invention also provides a process for the production of a protein having BTG activity which comprises culturing the above transformant.

The culturing conditions are not strictly limited and therefore can be suitably designed by those skilled in the art depending on the type of transformant to be desired.

For example, M9 CA₅₀ medium and M9 medium shown below can be used preferably for culturing *E. Coli* transformant.

M9 CA ₅₀		M9	
Casamino acid	2%	Na ₂ HPO ₄	0.6%
Glucose	0.4%	KH ₂ PO ₄	0.3%
0.8 mM MgSO ₄		NaCl	0.05%
L-Tryptophan	50 µg/ml	NH ₄ Cl	0.1%
Thiamine-HCl	0.5 µg/ml		
Ampicilline	50 µg/ml		

If necessary, expression of a gene of interest may be induced by adding an expression inducer such as IPTG (isopropyl-β-D-thiogalactopyranoside) to the culture medium used.

The thus expressed protein may be isolated and purified from culture filtrate, periplasm or cytoplasm of the host cells using various prior art means (cf. Protein Purification - Principles and Practice, Robert K. Scopes, Springer-Verlag, New York (1982); D. Koshland and D. Bostein, Cell, **20**, 749 (1980); and R.A. Hitzeman et al., Science, **219**, 620 (1983), etc.).

Examples of the present invention are given below by way of illustration but are not to be construed as limiting the present invention. Unless otherwise indicated, all parts, percents, ratios and the like are by weight.

EXAMPLE 1: Cloning of BTG gene

(1) Preparation of Cells

An actinomycete, Streptovercillium sp. was cultured at 30°C for 5 days in the following medium.

GP Medium	
Glycerol	0.4 wt%
Peptone	0.1 wt%
Yeast Extracts	0.4 wt%
MgSO ₄	0.05 wt%
KH ₂ PO ₄	0.2 wt%
Na ₂ HPO ₄	0.5 wt%
Glycine	0.1 wt%/l liter

(2) Preparation of DNA from Cells

A 400 ml portion of the cultured broth obtained above was centrifuged at 12,000 x g and at 4°C for 10 minutes, and the resulting pellet (cells) was suspended in a solution consisting of 50 mM Tris-HCl (pH 8.0), 5 mM EDTA and 50 mM NaCl (hereinafter, referred to as "TES"). The cell suspension thus prepared was centrifuged at 1,100 x g at room temperature for 10 minutes, and the resulting pellet (cells) was suspended in 5 ml of TES which had been supplemented with 2 mg/ml of lysozyme (Sigma Chemical Co.). After incubating the cell suspension at 37°C for 1 hour, the resulting lysate was frozen rapidly in acetone-dry ice and then suspended thoroughly in 42 ml of a solution consisting of 100 mM Tris-HCl (pH 9.0), 1% SDS and 100 mM NaCl (hereinafter, referred to as "Tris-SDS"). The resulting suspension was incubated at 60°C for 20 minutes, followed by immediate freezing in acetone-dry ice for 10 minutes. After re-incubation at 60°C, the resulting sample was extracted twice with phenol which has been saturated with Tris-SDS. Thereafter, two volumes of ethanol was added to the extract thus obtained, and filaments of DNA molecules formed in the mixture solution were recovered by winding them around a glass rod. DNA molecules thus recovered were washed with 80% ethanol, dried in a desiccator equipped with an aspirator and then dissolved in 5 ml of a solution consisting of 10 mM Tris-HCl (pH 8.0) and 1 mM EDTA (hereinafter, referred to as "TE").

Next, RNA in the thus prepared DNA sample was digested and removed. For this purpose, the DNA sample was dissolved in 5 ml of TE and was mixed with 0.5 ml of a solution consisting of 1 mg/ml of RNase A (Sigma Chemical Co.) and 2000 U/ml of RNase T1 (Boehringer-Mannheim Corp.). Then, the mixture was incubated at 37°C for 30 minutes. The incubated sample was extracted with a TE-saturated phenol/chloroform system and then with chloroform, and the water layer ultimately obtained was mixed with 1/10 volume of 3 M sodium acetate solution (pH 5.2) and 2 volumes of ethanol. After maintenance at -80°C for 30 minutes, the mixture was centrifuged at 12,000 x g and at 4°C for 15 minutes to recover a pellet which was then washed with 70% ethanol and dried. Thus obtained pellet of DNA (about 4 mg) was dissolved in 4 ml of TE for use in the following procedures.

(3) Preparation of DNA Fragment by PCR (polymerase chain reaction)

An appropriate DNA region containing BTG gene was isolated and amplified using a PCR technique (Saiki, R.F. et al., Science, vol. 230, pp. 1350 - 1354 (1985); and Mullis, K.B. and Faloona, F.A., Methods in Enzymology, vol. 155, pp. 335 - 350 (1987)).

(i) Synthesis of Primer DNA for PCR Use

Although BTG is known in the art, its amino acid sequence had not been known. The amino acid sequence of BTG

was determined for the first time at Shimonishi Laboratory of Protein Engineering Research Institute, Osaka University in collaboration with the present inventors.

A DNA fragment was synthesized based on a base sequence deduced from a portion of the determined amino acid sequence (from 117 position phenylalanine to 123 position phenylalanine) of BTG. In this instance, DNA synthesis was carried out using a Cyclone Plus DNA Synthesizer manufactured by Milligen Biosearch.

The DNA fragment thus obtained was designated Primer #1 for use in the PCR synthesis, and its sequence is shown below.

5'-TT_C^T GA_C^T GA_G^A GA_G^A AA_G^A GGI TT-3'

(20 mer, 32 mix, I (inosine) = 1)

(SEQ ID NO: 9)

Another DNA fragment was prepared in the same manner based on a base sequence deduced from a portion of the amino acid sequence (from position 325 lysine to position 331 proline). The DNA fragment thus obtained was designated Primer #2 for use in the PCR synthesis, and its sequence is shown below.

5'-GGC CAI CC_C^T TG_C^T TTI AC_C^T TT-3'

(20 mer, 8 mix; I (inosine) = 2)

(SEQ ID NO: 10)

Each of the thus prepared DNA fragments was dissolved in TE to a concentration of 20 μM.

(ii) Amplification of DNA Fragment using PCR

The amplification reaction was carried out using GeneAmp™ DNA Amplification Reagent Kit with AmpliTaq™ (produced by Perkin-Elmer Japan) and DNA Thermal Cycler (DNA amplifier, Perkin-Elmer Japan). The composition of the reaction solution used is shown below.

		(final conc.)	
5	H ₂ O	53.5 μ l	
	[10 x] Reaction Buffer (GeneAmp TM DNA Amplification Reagent Kit with AmpliTaq TM)	10 μ l	[1 x]
10	dNTPs, Mix 1.25 mM	16 μ l	200 μ M
	Primer #1 of (i)	5 μ l	1.0 μ M
15	Primer #2 of (i)	5 μ l	1.0 μ M
	Template (BTG DNA 0.5 μ g)*	10 μ l	
	AmpliTaq TM DNA Polymerase	0.5 μ l	2.5 U/assay
20	(total)	100 μ l	

25 *: The DNA obtained in (2) was dissolved in TE
to a concentration of 0.5 μ g/10 μ l.

30 After mixing 100 μ l of the above reaction solution with 100 μ l of mineral oil (Sigma Chemical Co.), a tube containing the resulting mixture was placed in the DNA Thermal Cycler (DNA amplifier, Perkin-Elmer Japan) to allow reaction under the following conditions.

95°C 1 min

35 37°C 2 min

72°C 3 min

40 The reaction was repeated 35 cycles under these conditions and then the final reaction mixture was incubated at 72°C for 7 minutes.

(iii) Recovery of Amplified DNA

45 After removing the mineral oil from the above reaction mixture, the remaining portion was mixed with 100 μ l of chloroform and centrifuged at 15,000 rpm for 2 minutes using a centrifuge manufactured by Tomy Seiko Co., Ltd. to recover 100 μ l of supernatant. Using a 10 μ l portion of the supernatant, the size and the amount of the recovered DNA were measured using 1.5% agarose gel electrophoresis. As a result, it was confirmed that a 645 bp DNA fragment was amplified to a level of about 2 μ g.

50 The remaining 90 μ l portion of the supernatant was subjected to 1.5% low melting point agarose electrophoresis to cut out a band corresponding to 645 bp. The band was dissolved at 65°C and mixed with the same volume of phenol. After centrifugation of the mixture, the resulting water layer was treated with phenol/ chloroform and chloroform in that order. The thus treated water layer was mixed with 3 M sodium acetate to a concentration of 8% and then with two volumes of ethanol, and the mixture was kept at -80°C for 15 minutes. Thereafter, the mixture was centrifuged at 15,000 rpm and at 4°C for 10 minutes to obtain a pellet which was then dissolved in 20 μ l of water. In this manner, about 1 μ g
55 of DNA fragments was recovered.

(4) Structure of DNA Fragment Amplified by PCR

In order to determine whether the DNA fragment thus amplified by PCR was a part of BTG gene, direct sequencing was carried out using 0.4 µg of the DNA fragment in the following manner. In this instance, the above-described Primer #1 was used as a primer for the sequencing.

Materials(i) Reagents for DNA Sequencing:

A sequencing kit, Sequenase™ (version 2.0), manufactured by USB Corp., USA, was used for the sequencing which was carried out basically by the dideoxy method (F. Sanger et al., *J. Mol. Biol.*, **143**, 161 (1980)).

(ii) Labeling of Primer for Sequencing Use:

Using a 2 pmol portion of Primer #1 prepared as in the foregoing for PCR reaction, its 5' end was labeled with [³²P] making use of T4 Kinase (TOYOBO Co., Ltd.). In this instance, [³²P] ATP having a specific activity of 3000 Ci/mmol was used. Free [³²P] ATP remaining in the labeled primer was removed by passing the product through an appropriate mini column (Sephadex G-50 DNA Grade Fine (Pharmacia)).

(iii) Reaction Solution (3.25 µl in total) for Sequencing:

Using the Sequenase™ kit, the following reaction mixture was prepared in each of four tubes for use in a G, A, T and C reaction.

2.5 µl	G, A, T, C termination mix
0.38 µl	5 x buffer (Sequenase™ (version 2.0))
0.22 µl	0.1 M DTT
0.15 µl	Sequenase (2 units)

Reaction

(i) A 0.4 µg portion of the amplified DNA and 2 pmol of [³²P]-labeled primer were dissolved in 12 µl of TE, and the solution was heat denatured at 95°C for 5 minutes, followed by rapid cooling in an ice bath.

(ii) Immediately after cooling, each of the four tubes was charged with 2.8 µl of the solution thus prepared in (i) above and then with 3.25 µl of corresponding sequence reaction solution (Sequenase™ (version 2.0)). After incubation of the thus prepared tubes at 37°C for 10 minutes, the reaction was terminated by adding 4 µl of a termination solution (Sequenase™ (version 2.0)) and heating at 75 to 80°C for 2 minutes, and the resulting samples were electrophoresed using a sequencing gel.

As a result of the direct sequencing, a base sequence encoding a portion of the amino acid sequence of BTG (from 129 position valine to 149 position asparagine) was found in the DNA fragment. As a result, this DNA fragment was considered to be a part of the BTG gene.

(5) Subcloning of PCR-Amplified DNA Fragment into pUC 19

Next, the DNA fragment amplified by PCR was subcloned into the SmaI site of pUC 19. For this purpose, both termini of the DNA fragment were made blunt-ended using the following procedure with a DNA Blunting Kit (Takara Shuzo Co., Ltd.).

(i) A micro-centrifugation tube was charged with a total of 9 µl of the following reaction-solution.

DNA Fragment 8 µl (0.4 µg)

10 x Buffer 1 µl

(ii) In order to prevent annealing at the DNA termini, the thus prepared tube was incubated at 70°C for 5 minutes and then transferred in a 37°C incubator.

(iii) A 1 µl portion of T4 DNA polymerase was transferred into the tube and the contents in the tube were mixed gently by pipetting.

(iv) The resulting mixture in the tube was incubated at 37°C for 5 minutes.

(v) A DNA dilution buffer (DNA Blunting Kit, Takara Shuzo Co., Ltd.) was added to the thus incubated mixture to a final concentration of 1 µg DNA/50 µl and the resulting mixture was stirred vigorously using a vortex mixer.

The thus blunt-ended DNA fragment was ligated with a SmaI digest of pUC 19, and *E. coli* DH 5α was transformed with the resulting ligate in the presence of 5-bromo-1-chloro-3-indolyl-β-D-galactoside (X-gal) and isopropyl-β-D-thiogalactoside (IPTG). A plasmid was isolated from an ampicillin-resistant white colony, in which the PCR-amplified DNA fragment was incorporated into the SmaI site of pUC 19. This plasmid was designated pUC 19 BTG and used in the following procedures. In this instance, ligation was carried out using a DNA Ligation Kit manufactured by Takara Shuzo Co., Ltd.

Next, in order to determine even wider range of the base sequence of the PCR-amplified DNA fragment, DNA sequencing was carried out using the thus obtained plasmid pUC 19 BTG as a template using a conventional method in which 7-deaza dGTPλ Sequenase kit of USB Corp. was used. As a result, a base sequence consisting of 564 base pairs was determined as shown in Table 9 below.

TABLE 9

```

TCCGTGATGAACAGGGCCCTGGAGAACGCCACGACGAGAGCGCTTACCTCGACAA
CCTCAAGAAGGAACTGGCGAACGGCAACGACGCCCTGCGCAACGAGGACGCCCCGTT
CCCCGTTCTACTCGGCGCTGCGGAACACGCCGTCTTTAAGGAGCGGAACGGAGGC
AATCACGACCCGTCCAGGATGAAGGCCGTCATCTACTCGAAGCACTTCTGGAGCGG
CCAGGACCGGTCGAGTTCGGCCGACAAGAGGAAGTACGGCGACCCGGACGCTTTC
GCCCCGCCCCCGGGACCGGCCCTGGTCGACATGTCGAGGGACAGGAACATTCCGCGC
AGCCCCACCAGCCCCGGTGAGGGATTTCGTCAATTTCTGACTACGGCTGGTTTCGGCGC
CCAGACGGAAGCGGACGCCGACAAGACCGTCTGGACCCACGGAAATCACTATCACG
CGCCCAATGGCAGCCTTGGTGCCATGCATGTATACGAGAGCAAGTTCCGCAACTGG
TCCGAAGGTTACTCCGACTTCGACCGCGGAGCCTATGTGATCACCTTCATCCCCAA
GAGC
(SEQ ID NO: 11)

```

(6) Preparation of DNA Library

(6-1) Partial Digestion of Chromosomal DNA of *Streptovorticillum* sp.

(a) A mixture of 24 µg of chromosomal DNA and 60 µl of BamHI 10 x buffer (10 x High Buffer of TOYOBO Co., Ltd.) was adjusted with sterile water to a total volume of 594 µl.

(b) The resulting mixture was pre-heated at 37°C for 5 minutes.

(c) The thus pre-heated mixture was further mixed with 6 µl of BamHI (TOYOBO Co., Ltd.) and the resulting mixture was incubated at 37°C for 10 minutes to complete the restriction enzyme reaction.

(d) The reaction was terminated by inactivating the restriction enzyme by heating the reaction mixture at 65°C for 15 minutes.

(6-2) Cloning (using EMBL3 Cloning Kit of Stratagene Cloning Systems)

(i) Ligation

(a) A 25 µl portion of the partially digested DNA obtained as described above was subjected to ethanol precipitation and the resulting precipitate was dissolved in 2.5 µl of TE.

(b) To this was added 1.0 µl of EMBL3 predigested arms (1 µg/µl), 0.5 µl of 10 x ligation buffer, 0.5 µl of 10 mM ATP (pH 7.5) and 0.5 µl of T4 DNA ligase (8 units/µl, product of Boehringer-Mannheim Corp.). After mixing, ligation was carried out at 4°C overnight. In this instance, the 10 x ligation buffer consisted of 500 mM Tris-HCl (pH 7.5), 70 mM MgCl₂ and 10 mM DTT.

(ii) Packaging (using Gigapack II Gold Packaging Extract, produced by Stratagene Cloning Systems)

(a) Appropriate portions of the sonic extract and freeze thaw lysate of the packaging kit stored in a freezer (-70°C) were put on dry ice, and the sonic extract was allowed to start melting.

(b) The freeze thaw lysate was warmed until it started to melt between the fingers.

(c) After adding 4 µl (1.6 µg on a DNA basis) of the above-described DNA solution, the freeze thaw lysate was put on an ice bath.

(d) Immediately thereafter, 15 µl of the sonic extract was added to the DNA-containing freeze thaw lysate.

(e) The resulting mixture was stirred to be mixed thoroughly without causing foams.

(f) The mixture was centrifuged at 4,000 x g for 5 seconds to precipitate all of the contents of the mixture in the tube.

(g) The resulting tube was incubated at room temperature (22°C) for 2 hours.

(h) To this was added 500 µl of a phage dilution buffer (prepared by dissolving 5.8 g of NaCl, 2.0 g of MgSO₄, 50 ml of 1 M Tris-HCl, pH 7.5, and 5 ml of 2% gelatin in 1 liter of water, followed by autoclaving).

(i) After adding 20 µl of chloroform, the resulting sample was mixed gently.

(j) The resulting mixture was centrifuged at 4,000 x g for 5 seconds to precipitate debris.

(k) The supernatant thus collected was stored at 4°C.

(iii) Plating

(a) E. coli P2392 was inoculated into TB medium which consisted of 5 g/l of NaCl and 10 g/l of Bactotryptone. Strain P2392 has the following properties: hsdR 514 (rk⁻, mk⁺), supE 44, supF 58, lacY 1, or Δ (lacZY), galK 2, galT 22, metB 1, trpR 55, (P2).

(b) P2392 thus inoculated in TB medium was cultured at 37°C with shaking.

(c) When the turbidity at OD₆₀₀ reached 0.5, the cells were collected by centrifugation at 1,100 x g for 15 minutes at room temperature, and subsequently suspended in an appropriate volume of 10 mM MgSO₄ solution to adjust the turbidity of the suspension to OD₆₀₀ = 0.5.

(d) The resulting cell suspension was mixed with a small portion of the supernatant obtained in (ii)-(k) above and incubated at 37°C for 15 minutes.

(e) The resulting suspension was mixed with 8 ml of a top agar which has been melted and warmed in advance, and the mixture was overlaid on an NZY plate.

Top Agar: NaCl 5 g/l, MgSO₄·H₂O 2 g/l, Yeast Extract 5 g/l, NZ Amine 10 g/l, Agarose 0.7%

NZY Plate: NaCl 5 g/l, MgSO₄·H₂O 2 g/l, Yeast Extract 5 g/l, NZ Amine 10 g/l, Agar 15 g/l

(f) The resulting plate was incubated overnight at 37°C.

As a result, a library of 3.0×10^4 independent clones was obtained.

(7) Screening of BTG Gene

Cloning of BTG gene was carried out using the library obtained in (6). Firstly, plating of phages in the library was

carried out in the same manner as the procedure in (6)-(iii). After culturing overnight at 37°C, lifting of phages was carried out from the thus formed plaques in the following manner.

- 5 (a) Each plate was maintained at 4°C for a few hours.
- (b) A nitrocellulose filter (S & S) was superposed on the surface of the plate (surface of the top agar).
- (c) The thus filter-covered plate was maintained as it is for about 2 minutes.
- (d) The nitrocellulose filter was removed from the plate and soaked for 1 minute in a solution which consisted of 0.5 M NaOH and 1.5 M NaCl.
- 10 (e) The thus treated nitrocellulose filter was soaked for 5 minutes in a solution which consisted of 1.5 M NaCl and 1 M Tris-HCl (pH 7.5).
- (f) The resulting nitrocellulose filter was then soaked for 30 seconds in 2 x SSC (1 x SSC consists of 0.15 M NaCl and 0.015 M sodium citrate and has a pH value of 7.0).
- (g) The thus soak-treated nitrocellulose filter was air-dried on a 3 MM filter paper.
- 15 (h) The nitrocellulose filter thus dried was held between two 3 MM filter papers and baked at 80°C for 2 hours.

Followed by phage lifting performed in this manner, hybridization was carried out using a probe which had been prepared by isolating a 650 bp fragment from EcoRI-HindIII digests of the plasmid pUC 19 BTG obtained in the foregoing manner and labeling the fragment with ³²P. This 650 bp fragment contained the entire portion of the DNA fragment which had been amplified by PCR. The ³²P-labeling was carried out using a multi-prime DNA labeling set manufactured by Amersham. The specific activity of the thus prepared probe was found to be 3 × 10⁸ cpm/μg DNA. Hybridization was carried out under the following conditions.

Pre-Hybridization:

25 Overnight incubation at 42°C in a hybridization solution consisting of 50% formamide, 1 x Denhardt's (0.02% BSA, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone), 0.1% SDS, 50 mM sodium phosphate buffer (pH 6.5) and 200 μg/μl denatured salmon sperm DNA.

30 Hybridization:

Overnight incubation at 42°C in the hybridization solution in the presence of 2 ng/ml of the probe. Washing:

- 35 1. 2 x SSC, 0.1% SDS, 5 minutes × 3 times, room temperature
2. 1 x SSC, 0.1% SDS, 1 hour × 2 times, 68°C

After washing, the nitrocellulose filter was air-dried and subjected to autoradiography.

By carrying out these steps, a total of about 40,000 plaques were screened (first screening) which resulted in the isolation of 16 clones having strong signals. Each of these clones was further subjected to a second screening to purify it into a single plaque. As a result, a total of 6 single plaque clones having strong signals were obtained.

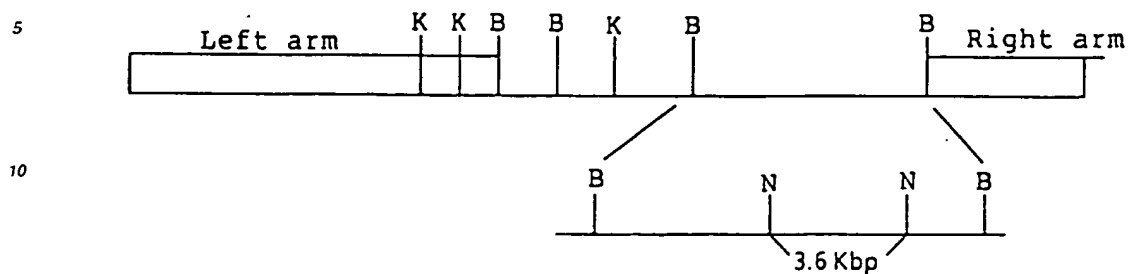
(8) Structural Analysis of Cloned DNA

45 In order to examine the DNA structures of the thus obtained 6 clones, DNA fragments were prepared from these clones in accordance with the method disclosed in Maniatis, Molecular Cloning, a Laboratory Manual, 2nd Edition.

Restriction enzyme digestion maps of the DNA fragments thus prepared were drawn up using restriction enzymes BamHI, SphI, NcoI, BglII and KpnI (all purchased from TOYOBO Co., Ltd.). As a result, it was found that these clones contained almost the same DNA fragment, and the restriction enzyme digestion map of the fragment was determined as follows.

50

55

λ BTG

K: KpnI, B: BamHI, N: NcoI

Next, Southern hybridization was carried out by digesting the DNA fragment with each restriction enzyme, isolating the digested fragments by electrophoresis, fixing the isolated fragments on a nitrocellulose filter and then hybridizing the fixed fragments with the probe used in the above-described BTG gene screening. The same hybridization conditions used for the screening of BTG gene were employed.

As a result, it was found that the 3.6 Kbp NcoI fragment of the above-described restriction enzyme digestion map hybridized with the probe and showed a strong signal. As a consequence, it was concluded that at least a portion of the BTG gene is contained in the NcoI fragment.

(9) Subcloning of 3.6 Kbp NcoI Fragment

Next, an attempt was made to subclone the 3.6 kbp NcoI fragment into a plasmid. The DNA fragment of the phage clone obtained as described above was digested with NcoI and a 3.6 Kbp DNA fragment was recovered by using a low melting point agarose. The thus obtained NcoI fragment was ligated with a DNA fragment which had been prepared by digesting plasmid pTV118N (Takara Shuzo Co., Ltd.) with NcoI, and *E. coli* DH 5 α was transformed with the thus ligated DNA sample. By culturing a transformant obtained in this way, a plasmid designated pTV118 NcoI was recovered in which the 3.6 kbp NcoI fragment had been subcloned into pTV118N.

(10) DNA Sequencing of BTG Gene

DNA sequencing was carried out using the thus obtained plasmid pTV118 NcoI as a template by repeating the process described in (4) above except that the reaction temperature was changed to 48°C and, depending on the degree of compression of the sequence, SSB (single stranded DNA binding protein, TOYOBO Co., Ltd.) was added to the reaction system. The base sequence thus determined is shown in the Table 10 below.

TABLE 10

5 TCGGGCGACGCGTAGGCAATGGGGGTTTCATCGCGACGTGCTTCCGCACGGCCGCGT
 TCAACGATGTTCCACGACAAAGGAGTTGCAGGTTTCCATGCGCTATACGCCGGAGG
 CTCTCGTCTTCGCCACTATGAGTGGGTTTATGCACCGCCGGATTTCATGCCGTGCG
 10 CCGGCGAGGCCGCCGCCGACAATGGCGCGGGGGAAGAGACGAAGTCCTACGCCGAA
 ACCTACCGCCTCACGGCGGATGACGTCGCGACATCAACGCGCTCAACGAAGCGCTC
 CGGCCGCTTCGAGCGCCGGCCCGTCGTTCCGGGCCCCCGACTCCGACGACAGGGTC
 15 ACCCTCCCGCCGAGCCGCTCGACAGGATGCCCGACCCGTACCGTCCCTCGTACGG
 CAGGGCCGAGACGGTCGTCAACAACCTACATACGCAAGTGGCAGCAGGTCTACAGCC
 20 ACCGCGACGGCAGGAAGCAGCAGATGACCGAGGAGCAACGGGAGTGGCTGTCCTAC
 GGCTGCGTCGGTGTACCTGGGTCAATTCGGGTCAGTACCCACGAACAGACTG¹GC
 CTTTCGCGTCCTTCGACGAGGACAGGTTCAAGAACGAGCTGAAGAACGGCAGGCCCC
 25 GGTCCGGCGAGACGCGGGCGGAGTTCGAGGGCCGCGTCGCGAAGGAGAGCTTTGAT
 GAAGAGAAGGGGTTCCAGCGGGCGCGTGAGGTGGCGTCCGTGATGAACAGGGCCCT
 30 GGAGAACGCCACGACGAGAGCGCTTACCTCGACAACCTCAAGAAGGAACTGGCGA
 ACGGCAACGACGCCCTGCGCAACGAGGACGCCCGTTCCCCGTTCTACTCGGCGCTG
 CGGAACACGCCGTCCTTTAAGGAGCGGAACGGAGGCAATCACGACCCGTCCAGGAT
 35 GAAGGCCGTCATCTACTCGAAGCACTTCTGGAGCGGCCAGGACCGGTCGAGTTTCGG
 CCGACAAGAGGAAGTACGGCGACCCGGACGCTTTCCGCCCCGGCCCCCGGGACCGGC
 40 CTGGTCGACATGTGAGGGACAGGAACATTCGCGCGAGCCCCACCAGCCCCGGTGA
 GGGATTTCGTCAATTTGACTACGGCTGGTTCGGCGCCCAGACGGAAGCGGACGCCG
 ACAAGACCGTCTGGACCCACGGAAATCACTATCACGCGCCCAATGGCAGCCTTGGT
 45 GCCATGCATGTATACGAGAGCAAGTTCGCAACTGGTCCGAAGGTTACTCCGACTT
 CGACCGCGGAGCCTATGTGATCACCTTCATCCCCAAGAGCTGGAACACCGCCCCCG
 50 ACAAGGTAAAGCAGGGCT¹²¹⁸TGGCCGTGATGTGAGCG
 (SEQ ID NO: 12)

55 The initiation codon of BTG gene was estimated to be the ATG moiety indicated as position 1 in the above base sequence, on the basis of the following three points: (1) a stop codon exists 81 bases upstream of position 1 and therefore the open reading frame of the BTG gene appears to start at downstream from this position; (2) a typical SD sequence (5'AAAGGAG-3') exists 13 bases upstream of the position 1 ATG; and (3) a region of about 20 amino acids from the position 1 ATG methionine is a signal sequence-like moiety which is relatively rich in hydrophobic amino acids.

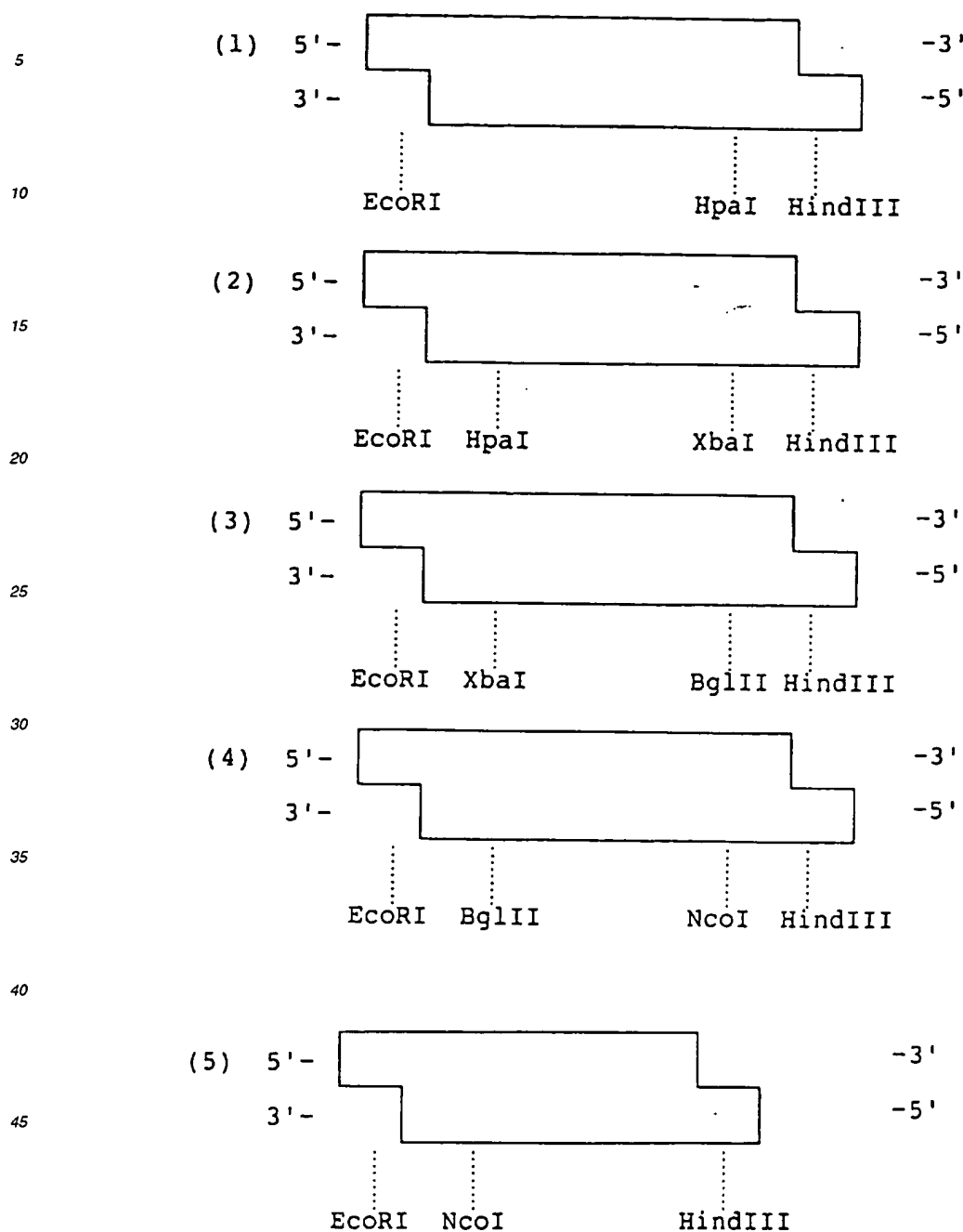
In addition, since a stop codon exists at position 1219 on the 3' end side, the position 1216 proline can be regarded as the C-terminus of the BTG gene. In the open reading frame deduced from the base sequence, the N-terminal amino acid of BTG determined by amino acid sequencing corresponds to the position 226 aspartic acid. As a result, it was found that the open reading frame of the BTG gene deduced herein had a structure consisting of the structure determined by the amino acid sequencing and additional 75 amino acids as follows:

TABLE 11

	-75	-70	-60	-50
	MRYTP	EALVFATMSA	VYAPPDSCRR	PARPPPTMAR
	-40	-30	-20	-10
	GKRRSPTPKP	TASRRMTSRH	QRAQRSAPAA	SSAGPSFRAP
10				
	10	20	30	40
	DSDDRVTTPA	EPLDRMPDPY	RPSYGRAETV	VNNYIRKWQQ
15				
	50	60	70	80
20	VYSHRDGRKQ	QMTEEQREWL	SYGCVGVTVV	NSGQYPTNRL
	90	100	110	120
	AFASFDEDRF	KNELKNGRPR	SGETRAEFEG	RVAKESFDEE
25				
	130	140	150	160
	KGFORAREVA	SVMNRALENA	HDESAYLDNL	KKELANGNDA
	170	180	190	200
30	LRNEDARSPF	YSALRNTPSF	KERNGGNHDP	SRMKAVIYSK
	210	220	230	240
	HFWSGQDRSS	SADKRKYGDP	DAFRPAPGTG	LVDMSRDRNI
	250	260	270	280
35	PRSPTSPGEG	FVNFDYGWFG	AQTEADADKT	VWTHGNHYHA
	290	300	310	320
	PNGSLGAMHV	YESKFRNWSE	GYSDFDRGAY	VITFIPKSWN
40				
	330			
	TAPDKVKQGW	P		
	(SEQ ID NO: 13)			

EXAMPLE 2: Chemical Synthesis of BTG Gene Design and Synthesis of BTG Gene

BTG gene DNA was designed based on the complete amino acid sequence thus determined by the foregoing analysis. In this instance, the utilization frequency of codons in *E. coli*, yeast and the like (Ikemura, T. and Ozeki, H., *Cold Spring Harbor Symp. Quant. Biol.*, vol. 47, p. 1087 (1983)) was taken into consideration, and restriction enzyme recognition sites were arranged on DNA chains of both ends of each of the fragments (1) to (5) for use in ligation of these fragments.



Next, the thus designed gene DNA was subjected to chemical synthesis by phosphoramidite technique using DNA Synthesizer 380A manufactured by Applied Biosystems.

The length of one DNA chain was set at around 30 to 40 bases, judging from the reliability and workability of currently used DNA synthesizers and DNA purification techniques. Since BTG consists of 331 amino acids, its corresponding gene requires at least 993 bases. Also, it is necessary to synthesize twice the amount of the gene DNA because the DNA must be incorporated into a plasmid as a double-stranded chain. In practice, however, it is necessary to introduce further a termination codon and restriction enzyme recognition sites for the ligation of each fragment. As a result, a total of 54 DNA chains as 27 pairs of double strands were synthesized. In addition, since the base sequence of the DNA chain must be confirmed after its incorporation into a plasmid, it may be convenient from handling point of view to split

the DNA into several fragments (about 200 bp for each) and incorporate such into respective plasmids, so that the base sequence can be determined safely.

In this procedure, therefore, the DNA chain was separated into 5 blocks each consisting of about 200 base pairs, the base sequence of each block incorporated into a plasmid was confirmed and then the complete BTG gene was constructed.

Construction of Synthetic Type BTG Gene

Firstly, construction of each fragment (about 200 bp) of the 5 blocks was carried out. Since the 5' end of a chemically synthesized oligonucleotide does not have phosphoric acid, phosphorylation of the 5' end was carried out using polynucleotide kinase. In this instance, phosphorylation of DNA chains on both 5' ends of each fragment was carried out after ligation.

100 pmol Oligonucleotide (dissolved in water)	7.5 μ l
10 x Buffer*	1 μ l
10 mM ATP	1 μ l
Polynucleotide Kinase (Takara Shuzo Co., Ltd.)	0.5 μ l (5 units)
(total)	10 μ l

*: 10 x buffer consisted of 650 mM Tris-HCl (pH 7.6), 100 mM $MgCl_2$, 150 mM dithiothreitol and 10 mM spermidine.

The above composition was transferred into an Eppendorf tube and incubated at 37°C for 1 hour and then boiled for 3 minutes to inactivate the enzyme. Next, a mixture of 5 μ l of a fragment with the same volume of its complementary fragment (10 μ l in total) was incubated at 90°C for 3 minutes in a water bath and then the water temperature in the bath was lowered spontaneously to 37°C to complete annealing. Thereafter, two DNA fragments (20 μ l) were ligated together.

Two DNA Fragment Pairs	20 μ l
150 mM Dithiothreitol (DTT)	2 μ l
10 mM ATP	2 μ l
Cloned T4 DNA Ligase (Takara Shuzo Co., Ltd.)	0.5 μ l (150 units)
(total)	24.5 μ l

The above composition was transferred into an Eppendorf tube and incubated at 16°C for 30 minutes. A 22 μ l portion of the resulting reaction solution was mixed with the same volume of an additional two reaction solutions obtained in the same manner (66 μ l in total), and 0.5 μ l of ligase was added to the mixture. After incubating the mixture at 16°C for 30 minutes, the resulting ligation solution was subjected to 10% polyacrylamide gel electrophoresis to recover a DNA fragment consisting of about 200 base pairs.

Each of the thus constructed DNA fragments (1) to (5) had an EcoRI recognition site on its 5' end and a HindIII recognition site on the 3' end. After phosphorylating both 5' ends of each DNA fragment, the resulting fragment was mixed with a plasmid pUC 18 (Yanisch-Perron, C. et al., Gene, vol. 33, p. 103 (1985)) which had been digested with EcoRI and HindIII in advance, and the mixture was subjected to a ligation reaction at 16°C for 1 hour using a DNA Ligation Kit (Takara Shuzo Co., Ltd.).

Next, E. coli JM 109 strain was transformed with each of the thus prepared ligation mixtures. This strain, JM 109, has the following characteristics: recA 1, Δ lac-pro, endA 1, gryA 96, thi-1, hsdR 17, supE 44, relA 1, λ^- , (F'traD 36,

proAB, lacI^qZAM15).

E. coli JM 109 strain is a strain which makes possible easy selection of recombinants when transformation of pUC-based plasmid DNA or transduction of M13 phage vector DNA is carried out, making use of reactivation of β -galactosidase by the action of lacZ α peptide produced by a vector DNA and lacZ Δ M15 encoded by JM 109 F'. In other words, when JM 109 strain is cultured on a medium containing IPTG (isopropyl- β -D-thiogalacto-pyranoside) and X-Gal (5-bromo-4-chloro-3-indole- β -D-galactoside), this strain forms a blue colony when it contains plasmid pUC 18 thus showing the presence of β -galactosidase activity, while this strain forms white colony when it contains a recombinant plasmid in which a foreign DNA fragment is incorporated because of its inability to reactivate β -galactosidase activity.

Plasmids were recovered from several white colonies and their DNA sequences were determined in accordance with the method of Sanger, F. et al., *J. Mol. Biol.*, vol. 143, p. 161 (1980). In this way, clones of interest were selected in which each inserted fragment showed the correct base sequence as has been designed.

Next, ligation of these DNA fragments was carried out making use of their respective restriction enzyme recognition sites.

Firstly, ligation of fragments (2) with (3) was carried out using BTG gene-containing Scal-XbaI fragments after digesting these fragments with Scal and XbaI making use of the Scal recognition site in the ampicillin resistant gene of pUC 18. In the same manner, ligation of fragments (4) with (5) was carried out using BTG gene-containing Scal-NcoI fragments after digesting these fragments with Scal and NcoI. Ligation of fragments (2), (3), (4) and (5) was carried out using BTG gene-containing Scal-BglII fragments after digesting the thus ligated products of (2) and (3) and of (4) and (5) with Scal and BglII.

Finally, an EcoRI-HpaI fragment of the DNA fragment (1) and a HpaI-HindIII fragment of the thus ligated sample of fragments (2), (3), (4) and (5) were mixed with a high expression/secretion vector for *E. coli* use, pIN-III-ompA2 (Ghrayeb, J. et al., *EMBO J.*, vol. 3, p. 2437 (1984)), which had been digested with EcoRI and HindIII in advance, and the resulting mixture was subjected to a ligation reaction at 16°C for 30 minutes using a DNA Ligation Kit (Takara Shuzo Co., Ltd.). The resulting reaction mixture was then incorporated into *E. coli* JA 221 strain (hsdM⁺, trpE 5, leuB 6, lacY, recA/F', lacI^q, lac⁺, pro⁺) (Nakamura, K. et al., *J. Mol. Appl. Genet.*, vol. 1, p. 289 (1982)). After culturing the thus treated cells, several plasmids were recovered from formed colonies, and examined as to whether the BTG gene (about 1 kb) was inserted correctly. A vector for use in the expression and secretion of BTG thus obtained was designated pOMPA-BTG. The base sequence of the chemically synthesized BTG gene, inserted into pIN-III-ompA2, is shown in Table 2.

The plasmid pIN-III-ompA2 used in this example contained a promoter (lppP) of *E. coli* outer membrane lipoprotein, a promoter and an operator (lacP^o) of lactose operon and a region for the signal peptide of *E. coli* outer membrane protein OmpA. As a result, expression of a gene incorporated into a downstream moiety of these regions is induced by the addition of IPTG, and the resulting genetic product is accumulated in the periplasm. Significant amounts of genetic products such as subtilisin in the periplasm have been reported, for instance, by Ikemura, H. et al., *J. Biol. Chem.*, vol. 262, p. 7859 (1987) and Hsiung, H.M. et al., *Bio/Technology*, vol. 4, p. 991 (1986). Purification of BTG protein may be effected by the conventional means of extracting periplasmic protein molecules making use of the osmotic pressure shock technique (Koshland, D. et al., *Cell*, vol. 20, p. 749 (1980) and then purifying the BTG protein by various biochemical techniques such as ammonium sulfate precipitation, ion exchange chromatography, gel filtration, HPLC and the like.

Not only pIN-III-ompA but also other expression plasmids may be used as the plasmid for use in the expression of the synthesized BTG gene. These other expression plasmids may easily be selected by those skilled in the art depending on the expression system to be used. For example, when an *E. Coli* strain is used as the host cell, commonly used vectors such as pTrc99A (Pharmacia); pPROK-C and pKK233-2 (Clontech Co.); and pNH8a, pNH16a, pNH18a, pcD-NAII, and pAX (Stratagene) can be used for the construction of an expression secretion vector of the present invention.

EXAMPLE 3: Expression of Synthetic BTG Gene

An *E. coli* JA 221 strain containing plasmid pOMPA-BTG in which the synthetic BTG gene had been incorporated (*E. Coli* AJ12569; BP-3558) was cultured in M9 casamino acid medium supplemented with 50 μ g/ml of ampicillin at 37°C for 2 hours with shaking, followed by additional culturing at 23°C for 4 hours in the presence of 1 mM IPTG. Cells were collected from 50 ml of the thus cultured broth by centrifugation and suspended in 2.5 ml of a solution consisting of 20% sucrose and 10 mM Tris-HCl (pH 7.5) to which was then added 0.125 ml of 0.5 M EDTA (pH 8.0). After keeping on ice for 30 minutes, the resulting cell suspension was centrifuged at 12000 rpm for 10 minutes to separate supernatant from cells. The resulting pellet or cells were suspended in 3 ml of distilled water, kept for 30 minutes on ice and then centrifuged at 12000 rpm for 10 minutes to separate supernatant from the cells. These supernatants were combined and ultracentrifuged at 38000 rpm for 60 minutes. The resulting supernatant was used as a periplasm fraction.

The cells remaining after centrifugation were suspended in 3 ml of distilled water, the suspension was subjected to ultrasonic disintegration (200 W, 5 minutes) and the resulting sample was used as a cytoplasm fraction.

Measurement of BTG Activity in Each Fraction

The BTG activity in each of the thus prepared fractions (culture filtrate, periplasm fraction and cytoplasm fraction) was measured using the hydroxamic acid method (colorimetric hydroxamate procedure according to the method of Folk and Cole).

The measurement was carried out, basically, according to the method of Folk and Cole (colorimetric hydroxamate procedure) disclosed in J. Biol. Chem., vol. 241, p. 5518, (1966). That is, the reaction was carried out using benzyloxy-carbonyl-L-glutamylglycine (CBZ-gln-gly) and hydroxylamine as the substrates in the presence or absence of Ca^{2+} . Hydroxamic acid thus formed was made into an iron complex in the presence of trichloroacetic acid. Thereafter, absorption of the iron complex was measured at 525 nm and the amount of hydroxamic acid was obtained from a calibration curve to calculate the activity of the sample.

<Measurement of Activity>Reagent A

0.2M Tris-HCl Buffer (pH 6.0)
0.1M Hydroxylamine
0.05 M Calcium Chloride
0.01 M Reduced Form Glutathione
0.03 M CBZ-gln-gly (Kokusan Kagaku Co., Ltd.)

Reagent B

3 N HCl	1 volume
12 % Trichloroacetic Acid	1 volume
5% $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$ (dissolved in 0.1 N HCl)	1 volume

A 0.4 ml portion of a sample (BTG as the enzyme solution) was mixed with 0.4 ml of Reagent A. After incubating the mixture at 37°C for 10 minutes, 0.4 ml of Reagent B was added to the resulting mixture to terminate the reaction and form an iron complex. Thereafter, absorption of the complex was measured at 525 nm.

As a control, an enzyme solution was inactivated by heating and subjected to the same reaction procedure, and its absorbance at 525 nm was subtracted from that of the active enzyme solution. A calibration curve was prepared using the same procedure except that γ -mono-hydroxamic acid L-glutamate was used instead of the enzyme solution. The amount of hydroxamic acid formed was calculated from the corrected absorbance using the thus prepared calibration curve. In this instance, one unit of the enzyme activity was defined as the amount of enzyme catalyzing the formation of one micromole of hydroxamic acid per minute under the above-described reaction conditions.

The following table shows the results obtained.

Samples	IPTG (mM)	BTG Activity (U/mg protein)
Culture Filtrate	-	0
	1	0.025
Periplasm Fraction	-	0
	1	0.22
Cytoplasm Fraction	-	0
	1	0.033

Though not so significant, BTG activities were detected in each of the samples when induced with IPTG.

In order to confirm the formation of the BTG gene product, an anti-BTG antibody was prepared in a rabbit using purified BTG and Western blotting was carried out making use of Vectastain ABC kit, produced by Vector Laboratories, Inc. in the following manner.

A 0.5 µl portion of each protein fraction was subjected to SDS-polyacrylamide gel electrophoresis and the resulting gel was transferred on a membrane filter (Immobilon, manufactured by Millipore Corp.) to fix the antigen protein on the filter. Thereafter, Western blotting was carried out using the rabbit anti-BTG antibody (1000 times dilution of a stock having an antibody titer of 64) to confirm product of the BTG gene at the protein level.

In this instance, the protein samples were applied to the SDS-polyacrylamide gel in the following order or lanes.

- 1: purified BTG (control)
- 2: culture filtrate (IPTG not added)
- 3: culture filtrate (IPTG 1 mM added)
- 4: periplasm fraction (IPTG not added)
- 5: periplasm fraction (IPTG 1 mM added)
- 6: cytoplasm fraction (IPTG not added)
- 7: cytoplasm fraction (IPTG 1 mM added)

As a result, colored bands were observed at the same position in lanes 1, 3, 5 and 7. In other words, protein reacted with the anti-BTG antibody was detected in every IPTG-added fraction at the same position which was equivalent to the molecular weight of the purified BTG.

Thus, it is apparent, in accordance with the present invention, a DNA gene has been provided which encodes transglutaminase, a plasmid in which the gene is incorporated, a transformant transformed with the plasmid and a process for the production of transglutaminase that comprises culturing the transformant.

EXAMPLE 4: Expression of BTG Gene (natural) in Actinomycetes

(1) Preparation of Plasmid Vector (pIJ 702)

Streptomyces lividans 3131 ATCC 35287 containing a plasmid pIJ 702 was cultured at 30°C for 2 days using the following medium.

YEME medium + 0.5 % glycine + 50 µg/ml thiostrepton	
0.3%	Yeast Extracts
0.5%	Peptone
0.3%	Malt Extracts
0.1%	Magnesium Chloride
1.0%	Glucose
34.0%	Sucrose
0.5%	Glycine
0.1%	50 mg/ml thiostrepton solution (sigma Chemical Co.; dimethyl sulfoxide solution) (total 1 liter, pH 7.0)

A 200 ml portion of the thus cultured broth was centrifuged at 12,000 x g and at 4°C for 10 minutes, and the resulting pellet (cells) was washed by suspending the cells in a solution consisting of 50 mM Tris-HCl (pH 8.0), 5 mM EDTA and 50 mM NaCl and centrifuging at 13,000 x g for 5 minutes at room temperature. The thus washed cells were suspended in 10 ml of a solution consisting of 50 mM Tris-HCl (pH 8.0), 10 mM EDTA and 25% sucrose (hereinafter, referred to as "TE-Sucrose"). The resulting cell suspension was mixed with 2 ml of TE-Sucrose containing 30 mg/ml of lysozyme (Sigma Chemical Co.) and 4 ml of 0.25 M EDTA, and the mixture was incubated at 37°C for 30 minutes. To this were then added 2 ml of 20% SDS and 5 ml of 5 M NaCl in that order. After stirring gently, the resulting mixture was incubated overnight at 0°C. The resulting cell lysate was centrifuged at 100,000 x g and at 4°C for 40 minutes, and the supernatant thus obtained was mixed with a 30% solution of polyethylene glycol 6000 (final concentration, 10%). After incubating at 0°C for 4.5 hours, the resulting mixture was centrifuged at 900 x g and at 4°C for 5 minutes, and the precipitate thus obtained was dissolved in a solution consisting of 10 mM Tris-HCl (pH 8.0), 1 mM EDTA and 50 mM NaCl. To this were added 16.8 g of cesium chloride and 1.2 ml of a solution consisting of 10 mM Tris-HCl (pH 8.0) and 1 mM EDTA (hereinafter, referred to as "TE") in which ethidium bromide has been dissolved to a concentration of 10 mg/ml. The resulting mixture was centrifuged at 1,300 x g for 15 minutes at room temperature to remove debris and then at 230,000 x g for 12 hours at 20°C. Thereafter, a layer containing plasmid DNA was separated from the centrifugation tube by

detecting the layer with ultraviolet light. In order to remove ethidium bromide, the thus obtained plasmid DNA was extracted three times with butanol which had been saturated with TE, followed by overnight dialysis against TE at 4°C. The thus dialyzed sample was extracted once with TE-saturated phenol and then twice with a chloroform/isoamyl alcohol system. To this were added 1/10 volume of 3 M sodium acetate (pH 5.2) and 2 volumes of ethanol. After standing for 30 minutes at -80°C, the resulting mixture was centrifuged at 12,000 x g for 15 minutes at 4°C. The precipitate thus recovered was washed with 70% ethanol, dried and then dissolved in 200 µl of TE. In this manner, about 10 µg of DNA was obtained.

(2) Preparation of Host Cells

Streptomyces lividans 3131 containing plJ 702 was cultured at 30°C for 7 days using YEME medium. The resulting culture broth was diluted with YEME medium to a degree of 10⁵ to 10⁹, and a 100 µl portion of each of the thus decimally diluted samples was inoculated on each of five plates containing YEME agar medium (YEME medium supplemented with 1.5% agar). After culturing at 30°C for 7 days, colonies formed on the plate medium were replicated on YEME agar medium containing 200 µg/ml of thiostrepton making use of RepliPlate™ Colony Transfer Pad (Takara Shuzo Co., Ltd.), and the thus replicated colonies were cultured again at 30°C for 7 days. A thiostrepton-sensitive strain Streptomyces lividans 3131-TS isolated in this manner was used as the host.

(3) Preparation of Streptomyces lividans3131-TS Protoplasts

The thiostrepton-sensitive strain of Streptomyces lividans 3131-TS obtained as in (2) above was cultured at 30°C for 2 days using the YEME + 0.5% glycine medium. A 200 ml portion of the resulting culture broth was centrifuged at 1,300 x g for 10 minutes at room temperature, and the cells thus precipitated were suspended in 72 ml of 0.35 M sucrose solution. The cell suspension was centrifuged at 1,300 x g for 10 minutes at room temperature, and the thus precipitated cells were suspended in 60 ml of buffer solution P containing 1 mg/ml of lysozyme (Sigma Chemical Co.). After incubating at 30°C for 2.5 hours, the resulting suspension was filtered through absorbent cotton to remove debris. A filtrate thus obtained was centrifuged at 1,300 x g for 10 minutes at room temperature, and protoplasts thus precipitated were washed twice with 25 ml of buffer solution P by centrifugation. Thereafter, the thus washed precipitate was suspended in 1 ml of buffer solution P to obtain a protoplast suspension. Buffer solution P used herein was prepared as follows.

	TES [N-Tris(hydroxymethyl)methyl-2-aminoethane sulfonic acid]	5.73 g
5	Sucrose	103 g
	Magnesium Chloride	2.03 g
10	Potassium Sulfate	0.5 g
	Calcium Chloride	3.68 g
	Trace Element Solution *	2 ml
15	Total	1 liter (pH 7.4)

* Trace Element Solution (per liter)

20	Zinc Chloride	40 mg
	Ferric Chloride	200 mg
	Cupric Chloride	10 mg
25	Manganese Chloride	10 mg
	Sodium Tetraborate	10 mg
30	Ammonium Molybdate	10 mg

In this instance, a 1% potassium dihydrogenphosphate solution was separately prepared and a 1 ml portion of the solution was added to 100 ml of buffer solution P prior to use.

(4) Construction of Actinomycetes Expression Type BTG Gene Fragment (Mp-BTGspm)

Since DNA sequencing results indicated that the BTG gene would form a prepro body, it was considered that processing of a precursor into a mature form would be effected smoothly by expressing the gene in Streptomyces lividans 3131-TS which belongs to the same actinomycetes family as in the case of the BTG-producing Streptovorticillium sp., rather than expressing it in other microorganisms. As a result, an expression type BTG gene fragment was constructed in the following manner.

i) Preparation of fragment containing signal, pro and structural sequences of BTG gene

A fragment containing signal, pro and structural sequences of BTG gene (hereinafter, referred to as "BTGspm fragment") was obtained using PCR technique using a 3.6 Kbp NcoI fragment of BTG gene as a template. Sequences of Primer #3 and Primer #4 used for the PCR procedure were as follows.

Primer #3

5' -ACGAGCTCAAAGGAGTTGCAGGTTTCCATGCGCTAT-3'

SacI

(36 mer)

(SEQ ID NO: 14)

Primer #4

5' - CCGGATCC AGATCT CACATCACGGCCAGCCCTGCTT - 3' (36 mer)
 | |
 BamHI BglII
 (SEQ ID NO: 15)

The PCR technique is already described in detail in Example 1 above for the procedures below.

ii) Preparation of fragment of *mel* (melanin synthesis gene) promoter region

The *mel* gene was selected as an expression promoter of the BTG gene, and a fragment of *mel* gene promoter region (referred to as "Mp fragment" hereinafter) was prepared by PCR using pIJ 702 as a template. The Primer #5 and Primer #6 sequences used for the PCR procedures were as follows.

Primer #5

5' - ACGAGCTCGTTGGGTTGACGACCCCG - 3' (26 mer)
 |
 SacI
 (SEQ ID NO: 16)

Primer #6

5' - ACGAATTCTGCAGTTTTCGCACGTGAGCCA - 3' (30 mer)
 | |
 EcoRI PstI
 (SEQ ID NO: 17)

iii) Construction of BTG gene fragment (Mp-BTGspn)

Each of the Mp fragment thus amplified by PCR and plasmid pUC 19 was digested with EcoRI and SacI (TOYOBO Co., Ltd.), and digested fragments having appropriate sizes of interest (about 260 bp and about 2700 bp, respectively) were recovered by low melting point agarose electrophoresis. After ligating the thus recovered fragments, *E. coli* DH α was transformed with the resulting ligate in the presence of X-gal and IPTG to isolate an ampicillin-resistant white colony. A plasmid recovered from the colony, in which the Mp fragment was inserted into the EcoRI-SacI site of pUC 19, was designated pUC19-Mp and used in the following procedures.

Each of the BTGspn fragment amplified by PCR in the same manner and the pUC19-Mp thus obtained were digested with BamHI and SacI (TOYOBO Co., Ltd.) and subjected to subcloning. A plasmid in which the BTGspn fragment was inserted into the BamHI-SacI site of pUC19-Mp was designated pUC19-Mp-BTGspn and used in the following procedures.

The plasmid pUC19-Mp-BTGspn thus prepared was treated with PstI and BglII (TOYOBO Co., Ltd.) to obtain a Mp-BTGspn fragment consisting of 1.4 kilo base pairs (Kbp). In these experiments, a DNA Ligation Kit manufactured by Takara Shuzo Co., Ltd. was used.

(5) Incorporation of BTG Gene into *Streptomyces lividans* 3131-TS

The 1.4 Kbp Mp-BTGsp^m fragment obtained above was ligated with a 5.1 Kbp PstI-BglII fragment of pIJ 702. The ligation was carried out by incubating the following reaction mixture overnight at 4°C.

1.4 Kbp Mp-BTGsp ^m Fragment	8.5 µl (ca. 500 ng)
5.1 Kbp pIJ702 PstI-BglII Fragment	8.5 µl (ca. 500 ng)
5 units/µl T4 DNA Ligase (Boehringer)	1.0 µl
10 x Ligation Buffer (Boehringer)	2.0 µl

After incubation, *Streptomyces lividans* 3131-TS was transformed with the thus ligated DNA in the following manner.

(a) The following reaction mixture was prepared and the total volume was adjusted to 140 µl.

DNA Solution	20 µl
<i>Streptomyces lividans</i> 3131-TS Protoplasts	100 µl
0.35 M Sucrose	20 µl

(b) A 1.5 ml portion of buffer solution P containing 20% polyethylene glycol 1000 was added to the reaction mixture and mixed gently by pipetting.

(c) The resulting mixture was allowed to remain still for 2 minutes at room temperature.

(d) The mixture was then centrifuged at 1,700 x g for 10 minutes at room temperature to collect pellet.

(e) The thus obtained pellet was washed twice with buffer solution P by centrifugation.

(f) The washed pellet was suspended in 1 ml of buffer solution P, and a 200 µl portion of the suspension was inoculated on an R-2 medium. In this instance, medium compositions R-2/A and R-2/B as shown below were prepared separately, and the R-2 medium was prepared by mixing these two compositions together with 1% KH₂PO₄ solution (1 ml per 200 ml final volume).

R-2/A (per 1 liter)	
Potassium Sulfate	0.5 g
Magnesium Chloride	20.2 g
Calcium Chloride	5.9 g
Glucose	20.0 g
Proline	6.0 g
Casamino Acid	0.2 g
Trace Element Solution	4 ml
Agar	44.0 g

R-2/B (per 1 liter, pH 7.4)

TES 11.5 g

Yeast Extracts 10.0 g

Sucrose 203 g

(g) The thus inoculated plates were incubated at 30°C for 18 hours.

(h) The entire surface of the plate medium was covered with 1 ml of buffer solution P containing 200 µg/ml of thiostrepton and 400 µg/ml of tyrosine.

(i) The resulting plates were further incubated at 30°C for 7 days to isolate thiostrepton-resistant white colonies. In this instance, a cell containing pIJ 702 in which a foreign DNA fragment was not inserted forms a black colony due to melanin synthesis by the mel gene.

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Plasmids were recovered from several white colonies thus isolated, and checked for the presence of inserted BTG gene. A BTG expression secretion vector thus obtained was designated pIJ702-BTG.

(6) Expression of BTG Gene

Streptomyces lividans AKW-1 was transformed with the thus obtained BTG gene-incorporated expression vector pIJ702-BTG and the resulting transformant was cultured at 30°C for 5 days using a medium having the following composition.

Polypeptone	2%
Soluble Starch	2%
Yeast Extracts	0.2%
K_2HPO_4	0.2%
$MgSO_4$	0.1%
Adekanol LG126	0.05%
50 mg/ml thiostrepton solution	0.1%

A 100 ml portion of the thus obtained culture broth was centrifuged at 12,000 x g for 10 minutes at 4°C, and the resulting supernatant fluid was concentrated by a factor of about 17 using an ultrafiltration membrane (nominal molecular weight cutoff of 1,000; Amicon Corp.).

Next, the amount of BTG in the thus prepared sample was measured by the EIA (enzyme immunoassay) method making use of an anti-BTG antibody preparation obtained in rabbit using purified BTG. As a result, about 0.1 mg/l of the BTG was detected. In this instance, the EIA was carried out in the following manner.

(a) A 50 µl portion of a sample was mixed with 500 µl of buffer A. After adding a single antibody-linked bead (beads were prepared from polystyrene #80 manufactured by Sekisui) thereto, the mixture was incubated at 37°C for 30 minutes.

(b) The bead was removed from the thus incubated mixture and washed twice with 10 mM phosphate buffer (pH 7.0).

(c) A 500 µl portion of a β-galactosidase-labeled antibody preparation (50 mu/500 µl buffer A) was added to the thus washed bead and incubated at 37°C for 30 minutes.

(d) The bead was removed from the thus incubated mixture and washed twice with 10 mM phosphate buffer (pH 7.0).

(e) A 500 µl portion of CPRG was added to the thus washed bead and incubated at 37°C for 30 minutes.

(f) After terminating the reaction with 2 ml of a stop solution, the absorbance at 575 nm was measured.

Buffer A	
0.1 M	Sodium Chloride
0.1%	BSA
1 mM	Magnesium Chloride
0.1%	Sodium Azide
10 mM	Phosphate Buffer (pH 7.0)

CPRG (per 1 liter, pH 5.0)

CPRG (chlorophenol red β -D-galactopyranomide, Boehringer)	1 g
BSA	333.2 mg
KH_2PO_4	833.2 mg
Na_2SO_3	166.8 mg
GH	333.2 ml

GH	
5%	Hydrolyzed Gelatin
0.3 M	Sodium Chloride
1 mM	Magnesium Chloride
0.1%	Sodium Azide
0.1%	BSA
50 mM	Phosphate Buffer (pH 7.0)

Stop Solution	
10 mM	EDTA-2H ₂ O
1%	Galactose
0.1%	Sodium Azide
50 mM	Phosphate Buffer (pH 7.0)

The recombinant BTG was then analyzed by Western blotting. The Western blotting results are shown in the accompanying Figure. Firstly, a sample was treated in the usual way prior to subjecting it to SDS-PAGE. After the electrophoresis, the protein present in the gel was transferred to a membrane (Immobilon™, Millipore Corp.) using an Electrophoretic Transfer Kit (LKB Instruments, Inc.) under the transfer conditions described in the instructions attached to the kit. The protein-transferred membrane was incubated for 1 hour in 10 ml of a blocking buffer consisting of 20 mM Tris-HCl (pH 7.9) and 5% skim milk and then overnight at 4°C in 10 ml of a solution of BTG antiserum which has been diluted by a factor of 200 with a rinse buffer consisting of 10 mM Tris-HCl (pH 7.9), 0.15 M NaCl, 0.1 mM EDTA (3 Na), 0.25% skim milk and 0.01% NaN_3 . After washing twice with the rinse buffer (20 ml for each), the thus incubated and washed membrane was incubated at 4°C for 4 hours in 10 ml of the rinse buffer containing 1 μCi of anti-rabbit ^{125}I -labeled whole antibody (Amersham). Thereafter, the thus incubated membrane was washed twice with the rinse buffer (20 ml for each), air-dried and then subjected to autoradiography.

As a result, BTG as a mature protein was found at a position of about 37 kilo daltons (KDa), a position equivalent to the molecular weight of the purified BTG, indicating that mature BTG protein was secreted by normal processing in spite of the introduction of a precursor gene into the expression system of BTG gene in Streptomyces lividans AKW-1.

EXAMPLE 5: Expression of BTG Gene (Synthetic) in Yeast

For expression of BTG gene in yeast, at a 3' end site of the signal sequence gene in an expression vector the BTG mature gene or with a ligated sequences of a BTG pro-sequence gene and BTG mature gene was inserted.

An E. coli-yeast shuttle vector pNJ 1053 which contains a promoter sequence of enolase gene (ENO 1) involved in the glycolytic pathway was used as the expression vector, because this sequence shows a strong promoter activity in yeast. For example, the ENO 1 promoter has been used for the expression of a human lysozyme gene and the like

in yeast cells as disclosed for instance by Ichikawa, K. et al. in Agric. Biol. Chem., vol. 53, p. 2687 (1989). This vector is a high copy type (YEp) vector which simultaneously contains pBR322-derived E. coli replication origin and ampicillin resistance gene, yeast 2 μ m replication origin and LEU 2 gene as a selection marker.

As the signal sequence, a human gastrin signal sequence (Kato, K. et al., Gene, vol. 26, pp. 53-57, (1983)) was used. This signal sequence, which consists of 21 amino acid residues and in which the carboxyl terminal side of its 21 position alanine is cut by the action of signal peptidase, has been employed in yeast cells for the expression and secretion of various foreign proteins such as human α -amylase (Sato, T. et al., Gene, vol. 83, pp. 355-365, (1989)).

As is known in Bacillus subtilis, a pro-sequence which is interposed between a signal sequence and a mature gene sequence assumes to have an important role in the expression of the activity of translated protein (Ikemura, H. et al., J. Biol. Chem., vol. 262, pp. 7859-7864 (1987); and other reports). The term "BTG pro-sequence" as used herein means a sequence of 39 amino acid residues starting from the -39 position lysine to the -1 position proline located downstream of the BTG signal-like sequence as shown in Example 1.

(1) Construction of Mature BTG Expression/Secretion Vector pNJ1053-BTG

A XhoI-HindIII fragment which consists of about 90 base pairs and contains a signal sequence-encoding gene was cut out from a gastrin signal sequence-containing vector (Sato, T. et al., Gene, vol. 83, pp. 355-365, (1989)) and inserted into a vector pHSG 396 (Takara Shuzo Co., Ltd.; Takeshita, S. et al., Gene, vol. 61, pp. 63-74, (1987)) which had been digested in advance with XhoI and HindIII to obtain a plasmid pHSG396-GS. A HindIII-digested fragment of this plasmid was ligated in series with a synthetic oligonucleotide consisting of about 30 base pairs (bp) as shown below and a PvuII-HindIII fragment (ca. 1 Kb) of the BTG gene chemically synthesized as in Example 2, in order to select a fragment in which mature BTG gene was inserted correctly into a downstream site of the signal sequence gene.

```

5'-AGCTTGGGAT TCTGATGACA GAGTCACTCC ACCAG-3'
3'-   ACCCTA AGACTACTGT CTCAGTGAGG TGGTC-5'

```

HindIII

PvuII

(SEQ ID NO: 18)

(SEQ ID NO: 19)

A Sall-HindIII region upstream of the XhoI recognition site of the thus selected fragment was cut out with corresponding restriction enzymes to obtain a fragment of about 1.1 kilo base pairs (Kbp). Thereafter, a Sall-HindIII region located on a downstream portion of the ENO 1 promoter of the yeast expression vector pNJ 1053 was replaced by the 1.1 Kbp fragment and the resulting plasmid was introduced into E. coli JM 109 to recover the titled expression/secretion vector pNJ1053-BTG.

(2) Construction of BTG Pro-sequence - Mature Protein Expression/Secretion Vector pNJ1053-proBTG

Firstly, synthesis of a gene which encodes a BTG pro-sequence region was carried out. In this instance, the utilization frequency of codons in E. coli, yeast and the like was taken into consideration, and restriction enzyme recognition sites were arranged for use in the ligation of the signal sequence gene and mature gene. That is, as shown below, the 5' end of the pro-sequence gene was arranged with a HindIII cohesive end sequence for use in its ligation with signal sequence gene, and the 3' end with a PvuII blunt end sequence for use in its ligation with the PvuII recognition site of the chemically synthesized BTG gene as in Example 2.

5' - AGCTTGGAGAGAGATCTCCAACTCCAAAGCCAACTGCTTCTAGAAGAATGACTTCTAGACACCAA
 3' - ACCTTCTCTCTAGAGGTTGAGGTTTCGGTTGACGAAGATCTTCTTACTGAAGATCTGTGGTT
 K R R S P T P K P T A S R R M T S R H Q
 10 20 30 40 50 60
 HindIII
 R A Q R S A P A A S S A G P S F R A P D
 AGAGCTCAAAGATCTGCTCCAGCTGCTTCTGCTGGTCCATCTTTCAGAGCTCCAGAT
 TCTCGAGTTTCTAGACGAGGTCGACGAAGAAGACGACGAGTAGAAAAGTCTCGAGGTCTA
 70 80 90 100 110 120
 S D D R V T P P (SEQ ID NO: 21)
 TCTGATGACAGAGTCACTCCACCAG -3' (SEQ ID NO: 20)
 AGACTACTGTCTCAGTGAGGTGTC -5' (SEQ ID NO: 22)
 130 140
 PvuII

Chemical synthesis of the BTG pro-sequence was carried out by firstly synthesizing a total of 6 oligonucleotide chains, each of which consisting of about 50 bases, as three pairs of double strands using a DNA synthesizer 380A manufactured by Applied Biosystems. The thus chemically synthesized oligonucleotides were phosphorylated, annealed and ligated in that order in the same manner as in the case of the chemical synthesis of BTG gene performed in Example 2. After these reactions, 10% polyacrylamide gel electrophoresis was carried out to recover a DNA fragment of about 150 base pairs from the gel. Next, in the same manner as in section (1) above, a HindIII-digested product of pHSG396-GS, the thus recovered 150 bp synthetic oligonucleotide and the PvuII-HindIII fragment (ca. 1 Kb) of the BTG gene chemically synthesized as in Example 2 were linked to one another in series, and a fragment in which the BTG pro-sequence gene was inserted correctly between the signal sequence and the BTG mature gene was selected. A Sall-HindIII region upstream of the XhoI recognition site of the thus selected fragment was cut out with the corresponding restriction enzymes to obtain a fragment of about 1.2 kilo base pairs (Kbp). Thereafter, a Sall-HindIII region located on a downstream portion of the ENO 1 promoter of the yeast expression vector pNJ 1053 was replaced by the 1.2 Kbp

fragment and the resulting plasmid was introduced into *E. coli* JM 109 to recover the titled expression/secretion vector pNJ1053-proBTG.

(3) Expression of BTG Gene in Yeast

Each of the expression/secretion vectors pNJ1053-BTG and pNJ1053-proBTG thus obtained in the sections (1) and (2) above was incorporated into a host yeast, *Saccharomyces cerevisiae* KSC22-1C (MATa, ssl 1, leu 2, his₋, ura 3), by means of an alkali metal treatment (Ito, H. et al., *J. Bacteriol.*, vol. 153, pp. 163-168, (1983)). In this instance, since it is necessary to use a minimum essential medium for the selection and culturing of a clone which has been transformed with a plasmid containing a gene compensating to an auxotrophic mutation, a 0.67% solution of bacto yeast nitrogen base (YNB) available from Difco Laboratories was used as the minimum medium by supplementing it with 2% glucose and, depending on the auxotrophic nature of the host yeast, with 20 mg/ℓ of L-histidine hydrochloride and 20 mg/ℓ of uracil (plus 2% agar in the case of a plate medium). Transformant cells which became Leu⁺ formed colonies when cultured on the plate medium at 30°C for 2 to 4 days.

Each transformant containing the expression/ secretion vector pNJ1053-BTG or pNJ1053-proBTG was cultured overnight in the minimum essential medium at 30°C to prevent plasmid deletion and then the resulting culture broth was inoculated (5% inoculum) into 10 ml of the following synthetic medium and cultured at 30°C for 2 days with shaking.

Synthetic Medium	
YNB	0.67%
Glucose	8%
L-Histidine Hydrochloride	20 mg/ℓ
Uracil	20 mg/ℓ
Casamino Acid (Difco)	0.5%

Next, a cell extract was prepared using the glass beads method (Hitzeman, R.A. et al., *Science*, vol. 219, pp. 620-625, (1983)). That is, cells were collected from 10 ml of the cultured broth by centrifugation, washed with sterile water and suspended in 1 ml of a Tris-HCl solution (pH 6.0). A 1 ml volume of glass beads (0.45-0.5 mm in diameter, manufactured by B. Brown) were added to the cell suspension and the mixture was shaken vigorously at 0 to 4°C for 1 minute on a vortex mixer. The shaking step was repeated three times. After removing the glass beads using a low speed centrifugation, the resulting supernatant was transferred into an Eppendorf tube. The tube was then centrifuged at 12,000 rpm for 5 minutes, and the resulting supernatant was used as a cell extract.

In order to confirm the production of the BTG gene product, an anti-BTG antibody was prepared in a rabbit using purified BTG and Western blotting was carried out using a Vectastain ABC kit (produced by Vector Laboratories, Inc.) in the following manner. A predetermined volume (about 1 µg, as total protein) of each extract of yeast cells containing the expression/ secretion vector pNJ1053-BTG or pNJ1053-proBTG was subjected to SDS-polyacrylamide gel electrophoresis and the resulting gel was transferred on a membrane filter (Immobilon, manufactured by Millipore Corp.) to fix the antigen protein on the filter. Thereafter, Western blotting was carried out using the rabbit anti-BTG antibody (1000 times dilution of a stock having an antibody titer of 64) to confirm the product of the BTG gene at the protein level.

In this instance, the protein samples were applied to an SDS-polyacrylamide gel in the following order or lanes.

- 1: purified BTG (control)
- 2: extract of yeast cells containing pNJ1053
- 3: extract of yeast cells containing pNJ1053-BTG (mature BTG gene)
- 4: extract of yeast cells containing pNJ1053-proBTG (BTG pro-sequence and mature BTG gene)

As a result, colored bands were observed at the same position in lanes 1, 3 and 4. In other words, protein reacted with the anti-BTG antibody was detected in every extract of yeast cells containing the BTG gene at the same position which was equivalent to the molecular weight of the purified BTG.

In this instance, the culture filtrates obtained during the process for the preparation of these cell extracts were also subjected to Western blotting, but no band corresponding to BTG was found. In the case of the yeast cells containing the expression/secretion vector pNJ1053-proBTG in which the BTG pro-sequence and mature BTG gene system had been incorporated, the appearance of a band corresponding to BTG in lane 4 at the same position of the purified BTG indicated that correct processing of the synthetic pro-sequence had occurred in the yeast cells.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

Amano Pharmaceutical
Co., Ltd., and
Ajinomoto Co, Inc

(ii) TITLE OF INVENTION: Recombinant transglutaminase

(iii) NUMBER OF SEQUENCES: 22

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.24

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: JP 2-282566
- (B) FILING DATE: 19-OCT-1990

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp 1	Ser	Asp	Asp 5	Arg	Val	Thr	Pro	Pro	Ala 10	Glu	Pro	Leu	Asp	Arg 15	Met
Pro	Asp	Pro	Tyr 20	Arg	Pro	Ser	Tyr	Gly 25	Arg	Ala	Glu	Thr	Val 30	Val	Asn
Asn	Tyr	Ile 35	Arg	Lys	Trp	Gln	Gln 40	Val	Tyr	Ser	His	Arg 45	Asp	Gly	Arg
Lys	Gln 50	Gln	Met	Thr	Glu	Glu 55	Gln	Arg	Glu	Trp	Leu 60	Ser	Tyr	Gly	Cys
Val 65	Gly	Val	Thr	Trp	Val 70	Asn	Ser	Gly	Gln	Tyr 75	Pro	Thr	Asn	Arg	Leu 80
Ala	Phe	Ala	Ser	Phe 85	Asp	Glu	Asp	Arg	Phe 90	Lys	Asn	Glu	Leu	Lys 95	Asn
Gly	Arg	Pro	Arg 100	Ser	Gly	Glu	Thr	Arg 105	Ala	Glu	Phe	Glu	Gly 110	Arg	Val
Ala	Lys	Glu 115	Ser	Phe	Asp	Glu	Glu 120	Lys	Gly	Phe	Gln	Arg 125	Ala	Arg	Glu
Val 130	Ala	Ser	Val	Met	Asn	Arg 135	Ala	Leu	Glu	Asn	Ala 140	His	Asp	Glu	Ser
Ala 145	Tyr	Leu	Asp	Asn	Leu 150	Lys	Lys	Glu	Leu	Ala 155	Asn	Gly	Asn	Asp	Ala 160
Leu	Arg	Asn	Glu	Asp 165	Ala	Arg	Ser	Pro	Phe 170	Tyr	Ser	Ala	Leu	Arg 175	Asn
Thr	Pro	Ser	Phe 180	Lys	Glu	Arg	Asn	Gly 185	Gly	Asn	His	Asp	Pro 190	Ser	Arg
Met	Lys	Ala 195	Val	Ile	Tyr	Ser	Lys 200	His	Phe	Trp	Ser	Gly 205	Gln	Asp	Arg
Ser	Ser 210	Ser	Ala	Asp	Lys	Arg 215	Lys	Tyr	Gly	Asp	Pro 220	Asp	Ala	Phe	Arg
Pro 225	Ala	Pro	Gly	Thr	Gly 230	Leu	Val	Asp	Met	Ser 235	Arg	Asp	Arg	Asn	Ile 240
Pro	Arg	Ser	Pro	Thr 245	Ser	Pro	Gly	Glu	Gly 250	Phe	Val	Asn	Phe	Asp 255	Tyr

Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp
 260 265 270
 5 Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met
 275 280 285
 His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp
 290 295 300
 10 Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn
 305 310 315 320
 Thr Ala Pro Asp Lys Val Lys Gln Gly Trp Pro
 325 330

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 GATTCTGATG ACAGAGTCAC TCCACCAGCT GAACCATTGG ATAGAATGCC AGATCCATAC 60
 AGACCATCTT ACGGTAGAGC TGAAACTGTT GTCAACAACCT ACATTAGAAA GTGGCAACAA 120
 GTCTACTCTC ACAGAGATGG TAGAAAGCAA CAAATGACTG AAGAACAAAG AGAATGGTTG 180
 30 TCTTACGGTT GTGTTGGTGT TACTTGGGTT AACTCTGGTC AATACCCAAC TAACAGATTG 240
 GCTTTCGCTT CTTTCGATGA AGATAGATTC AAGAACGAAT TGAAGAACGG TAGACCAAGA 300
 TCCGGTGAAA CTAGAGCTGA ATTCGAAGGT AGAGTTGCTA AGGAATCTTT CGATGAAGAA 360
 35 AAGGGTTTCC AAAGAGCTAG AGAAGTTGCT TCTGTTATGA ACAGAGCTCT AGAAAACGCT 420
 CACGATGAAT CTGCTTACTT GGATAACTTG AAGAAGGAAT TGGCCAACGG TAACGATGCT 480
 TTGAGAAACG AAGATGCTAG ATCCCCATTC TACTCTGCTT TGAGAAACAC TCCATCTTTC 540
 40 AAGGAAAGAA ACGGTGGTAA CCACGATCCA TCCAGAATGA AGGCTGTTAT TTA CTCTAAG 600
 CACTTCTGGT CTGGTCAAGA TAGATCTTCT TCTGCTGATA AGAGAAAGTA CGGTGATCCA 660
 45 GATGCTTTCA GACCAGCTCC AGGTACCGGT TTGGTCGACA TGTCCAGAGA TAGAAACATT 720

CCAAGATCCC CAACTTCTCC AGGTGAAGGT TTCGTCAACT TCGATTACGG TTGGTTCGGT 780
 GCTCAAACTG AAGCTGATGC TGATAAGACT GTTTGGACCC ATGGTAACCA CTACCACGCT 840
 5 CCAAACGGTT CTTTGGGTGC TATGCACGTC TACGAATCTA AGTTCAGAAA CTGGTCTGAA 900
 GGTTACTCTG ATTTGATAG AGGTGCTTAC GTTATTACTT TCATTCCAAA GTCTTGGAAC 960
 ACTGCTCCAG ACAAGGTCAA GCAAGGTTGG CCA 993

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACTCCGACG ACAGGGTCAC CCTCCCGCC GAGCCGCTCG ACAGGATGCC CGACCCGTAC 60
 CGTCCCTCGT ACGGCAGGGC CGAGACGTC GTCAACAACT ACATACGCAA GTGGCAGCAG 120
 25 GTCTACAGCC ACCGCGACGG CAGGAAGCAG CAGATGACCG AGGAGCAACG GGAGTGGCTG 180
 TCCTACGGCT GCGTCGGTGT CACCTGGGTC AATTCGGGTC AGTACCCAC GAACAGACTG 240
 GCCTTCGCGT CCTTCGACGA GGACAGGTTT AAGAACGAGC TGAAGAACGG CAGGCCCCGG 300
 30 TCCGGCGAGA CGCGGGCGGA GTTCGAGGGC CGCGTCGCGA AGGAGAGCTT TGATGAAGAG 360
 AAGGGGTTC AGCGGGCGCG TGAGGTGGCG TCCGTGATGA ACAGGGCCCT GGAGAACGCC 420
 CACGACGAGA GCGCTTACCT CGACAACCTC AAGAAGGAAC TGGCGAACGG CAACGACGCC 480
 35 CTGCGCAACG AGGACGCCCC TTCCCCGTTC TACTCGGCGC TCGGGAACAC GCCGTCCTTT 540
 AAGGAGCGGA ACGGAGGCAA TCACGACCCG TCCAGGATGA AGGCCGTCAT CTACTCGAAG 600
 CACTTCTGGA GCGGCCAGGA CCGGTCGAGT TCGGCCGACA AGAGGAAGTA CGGCGACCCG 660
 40 GACGCTTTCC GCCCGGCCCC CGGGACCGGC CTGGTCGACA TGTCGAGGGA CAGGAACATT 720
 CCGCGCAGCC CCACCAGCCC CGGTGAGGGA TTCGTCAATT TCGACTACGG CTGGTTCGGC 780
 GCCCAGACGG AAGCGGACGC CGACAAGACC GTCTGGACCC ACGGAAATCA CTATCACGCG 840
 45 CCCAATGGCA GCCTTGGTGC CATGCATGTA TACGAGAGCA AGTTCCGCAA CTGGTCCGAA 900

GGTTACTCCG ACTTCGACCG CGGAGCCTAT GTGATCACCT TCATCCCCAA GAGCTGGAAC 960

ACCGCCCCCG ACAAGGTAAA GCAGGGCTGG CCG 993

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Tyr Thr Pro Glu Ala Leu Val Phe Ala Thr Met Ser Ala Val
-75 -70 -65 -60

Tyr Ala Pro Pro Asp Ser Cys Arg Arg Pro Ala Arg Pro Pro Pro Thr
-55 -50 -45

Met Ala Arg Gly Lys Arg Arg Ser Pro Thr Pro Lys Pro Thr Ala Ser
-40 -35 -30

Arg Arg Met Thr Ser Arg His Gln Arg Ala Gln Arg Ser Ala Pro Ala
-25 -20 -15

Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro
-10 -5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Arg Arg Ser Pro Thr Pro Lys Pro Thr Ala Ser Arg Arg Met Thr
-39 -35 -30 -25

Ser Arg His Gln Arg Ala Gln Arg Ser Ala Pro Ala Ala Ser Ser Ala
-20 -15 -10

Gly Pro Ser Phe Arg Ala Pro
-5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCGCTATA CGCCGGAGGC TCTCGTCTTC GCCACTATGA GTGCGGTTTA TGCACCGCCG 60
 GATTCATGCC GTCGGCCGGC GAGGCCGGCG CCGACAATGG CGCGGGGGAA GAGACGAAGT 120
 CCTACGCCGA AACCTACCGC CTCACGGCGG ATGACGTCGC GACATCAACG CGCTCAACGA 180
 AGCGCTCCGG CCGCTTCGAG CGCCGGCCCC TCGTTCCGGG CCCCC 225

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGAGAAGAT CTCCAATCC AAAGCCAAC TCTTCTAGAA GAATGACTTC TAGACACCAA 60
 AGAGCTCAAA GATCTGCTCC AGCTGCTTCT TCTGCTGGTC CATCTTTCAG AGCTCCA 117

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGCGCTATA CGCCGGAGGC TCTCGTCTTC GCCACTATGA GTGCGGTTTA TGCACCGCCG 60

5 GATTCATGCC GTCGGCCGGC GAGGCCGCCG CCGACAATGG CGCGGGGGAA GAGACGAAGT 120
 CCTACGCCGA AACCTACCGC CTCACGGCGG ATGACGTCGC GACATCAACG CGCTCAACGA 180
 AGCGCTCCGG CCGCTTCGAG CGCCGGCCCG TCGTTCCGGG CCCCCGACTC CGACGACAGG 240
 GTCACCCCTC CCGCCGAGCC GCTCGACAGG ATGCCCCGACC CGTACCGTCC CTCGTACGGC 300
 10 AGGGCCGAGA CGGTCGTCAA CAACTACATA CGCAAGTGGC AGCAGGTCTA CAGCCACCGC 360
 GACGGCAGGA AGCAGCAGAT GACCGAGGAG CAACGGGAGT GGCTGTCCTA CGGCTGCGTC 420
 GGTGTCACCT GGGTCAATTC GGGTCAGTAC CCGACGAACA GACTGGCCTT CGCGTCCTTC 480
 15 GACGAGGACA GGTTC AAGAA CGAGCTGAAG AACGGCAGGC CCCGGTCCGG CGAGACGCGG 540
 GCGGAGTTCG AGGGCCGCGT CGCGAAGGAG AGCTTTGATG AAGAGAAGGG GTTCCAGCGG 600
 GCGCGTGAGG TGGCGTCCGT GATGAACAGG GCCCTGGAGA ACGCCACGA CGAGAGCGCT 660
 20 TACCTCGACA ACCTCAAGAA GGAAGTGGCG AACGGCAACG ACGCCCTGCG CAACGAGGAC 720
 GCGCGTTCCC CGTTCTACTC GCGCTGCGG AACACGCCGT CCTTTAAGGA GCGGAACGGA 780
 GGCAATCACG ACCCGTCCAG GATGAAGGCC GTCATCTACT CGAAGCACTT CTGGAGCGGC 840
 25 CAGGACCGGT CGAGTTCGGC CGACAAGAGG AAGTACGGC ACGCGACGC TTTCCGCCCC 900
 GCGCGCGGGA CCGGCCTGGT CGACATGTCG AGGGACAGGA ACATTCCGCG CAGCCCCACC 960
 AGCCCCGGTG AGGGATTCGT CAATTCGAC TACGGCTGGT TCGGCGCCCA GACGGAAGCG 1020
 30 GACGCCGACA AGACCGTCTG GACCCACGGA AATCACTATC ACGCGCCCA TGGCAGCCTT 1080
 GGTGCCATGC ATGTATACGA GAGCAAGTTC CGCAACTGGT CCGAAGGTTA CTCCGACTTC 1140
 GACCGCGGAG CCTATGTGAT CACCTTCATC CCCAAGAGCT GGAACACCGC CCGGACAAG 1200
 35 GTAAAGCAGG GCTGGCCG 1218

(2) INFORMATION FOR SEQ ID NO:9:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

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(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTYGAYGARG ARAARGGNTT

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCCANCCYT GYTTNACYTT

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCCGTGATGA ACAGGGCCCT GGAGAACGCC CACGACGAGA GCGCTTACCT CGACAACCTC

60

AAGAAGGAAC TGGCGAACGG CAACGACGCC CTGCGCAACG AGGACGCCCC TTCCCCGTTC

120

TACTCGGCGC TGCGGAACAC GCCGTCCTTT AAGGAGCGGA ACGGAGGCAA TCACGACCCG

180

TCCAGGATGA AGGCCGTCAT CTACTCGAAG CACTTCTGGA GCGGCCAGGA CCGGTCGAGT 240
 TCGGCCGACA AGAGGAAGTA CGGCGACCCG GACGCTTCC GCCCGGCCCC CGGGACCGGC 300
 5 CTGGTTCGACA TGTCGAGGGA CAGGAACATT CCGCGCAGCC CCACCAGCCC CGGTGAGGGA 360
 TTCGTCAATT TCGACTACGG CTGGTTCGGC GCCCAGACGG AAGCGGACGC CGACAAGACC 420
 GTCTGGACCC ACGGAAATCA CTATCACGCG CCCAATGGCA GCCTTGGTGC CATGCATGTA 480
 10 TACGAGAGCA AGTCCGCAA CTGGTCCGAA GGTACTCCG ACTTCGACCG CGGAGCCTAT 540
 GTGATCACCT TCATCCCCAA GAGC 564

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptovercillium sp.

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pTV118 NcoI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGCGGCGACG CGTAGGCAAT GGGGGTTCAT CGCGACGTGC TTCCGCACGG CCGCGTTCAA 60
 CGATGTTCCA CGACAAAGGA GTTGCAGGTT TCC ATG CGC TAT ACG CCG GAG GCT 114
 Met Arg Tyr Thr Pro Glu Ala
 -75 -70
 35 CTC GTC TTC GCC ACT ATG AGT GCG GTT TAT GCA CCG CCG GAT TCA TGC 162
 Leu Val Phe Ala Thr Met Ser Ala Val Tyr Ala Pro Pro Asp Ser Cys
 -65 -60 -55
 40 CGT CGG CCG GCG AGG CCG CCG CCG ACA ATG GCG CCG GGG AAG AGA CGA 210
 Arg Arg Pro Ala Arg Pro Pro Pro Thr Met Ala Arg Gly Lys Arg Arg
 -50 -45 -40
 45 AGT CCT ACG CCG AAA CCT ACC GCC TCA CGG CCG ATG ACG TCG CGA CAT 258
 Ser Pro Thr Pro Lys Pro Thr Ala Ser Arg Arg Met Thr Ser Arg His
 -35 -30 -25

EP 0 481 504 B1

5	CAA CGC GCT CAA CGA AGC GCT CCG GCC GCT TCG AGC GCC GGC CCG TCG Gln Arg Ala Gln Arg Ser Ala Pro Ala Ala Ser Ser Ala Gly Pro Ser -20 -15 -10 -5	306
	TTC CGG GCC CCC GAC TCC GAC GAC AGG GTC ACC CCT CCC GCC GAG CCG Phe Arg Ala Pro Asp Ser Asp Arg Val Thr Pro Pro Ala Glu Pro 1 5 10	354
10	CTC GAC AGG ATG CCC GAC CCG TAC CGT CCC TCG TAC GGC AGG GCC GAG Leu Asp Arg Met Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu 15 20 25	402
15	ACG GTC GTC AAC AAC TAC ATA CGC AAG TGG CAG CAG GTC TAC AGC CAC Thr Val Val Asn Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr Ser His 30 35 40	450
	CGC GAC GGC AGG AAG CAG CAG ATG ACC GAG GAG CAA CGG GAG TGG CTG Arg Asp Gly Arg Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Trp Leu 45 50 55 60	498
20	TCC TAC GGC TGC GTC GGT GTC ACC TGG GTC AAT TCG GGT CAG TAC CCC Ser Tyr Gly Cys Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro 65 70 75	546
25	ACG AAC AGA CTG GCC TTC GCG TCC TTC GAC GAG GAC AGG TTC AAG AAC Thr Asn Arg Leu Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn 80 85 90	594
	GAG CTG AAG AAC GGC AGG CCC CGG TCC GGC GAG ACG CGG GCG GAG TTC Glu Leu Lys Asn Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe 95 100 105	642
30	GAG GGC CGC GTC GCG AAG GAG AGC TTT GAT GAA GAG AAG GGG TTC CAG Glu Gly Arg Val Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln 110 115 120	690
35	CGG GCG CGT GAG GTG GCG TCC GTG ATG AAC AGG GCC CTG GAG AAC GCC Arg Ala Arg Glu Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn Ala 125 130 135 140	738
	CAC GAC GAG AGC GCT TAC CTC GAC AAC CTC AAG AAG GAA CTG GCG AAC His Asp Glu Ser Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn 145 150 155	786
40	GGC AAC GAC GCC CTG CGC AAC GAG GAC GCC CGT TCC CCG TTC TAC TCG Gly Asn Asp Ala Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser 160 165 170	834
45	GCG CTG CGG AAC ACG CCG TCC TTT AAG GAG CGG AAC GGA GGC AAT CAC Ala Leu Arg Asn Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His 175 180 185	882

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5 GAC CCG TCC AGG ATG AAG GCC GTC ATC TAC TCG AAG CAC TTC TGG AGC 930
 Asp Pro Ser Arg Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser
 190 195 200

GGC CAG GAC CGG TCG AGT TCG GCC GAC AAG AGG AAG TAC GGC GAC CCG 978
 Gly Gln Asp Arg Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro
 205 210 215 220

10 GAC GCT TTC CGC CCG GCC CCC GGG ACC GGC CTG GTC GAC ATG TCG AGG 1026
 Asp Ala Phe Arg Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser Arg
 225 230 235

GAC AGG AAC ATT CCG CGC AGC CCC ACC AGC CCC GGT GAG GGA TTC GTC 1074
 Asp Arg Asn Ile Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe Val
 240 245 250

15 AAT TTC GAC TAC GGC TGG TTC GGC GCC CAG ACG GAA GCG GAC GCC GAC 1122
 Asn Phe Asp Tyr Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp
 255 260 265

20 AAG ACC GTC TGG ACC CAC GGA AAT CAC TAT CAC GCG CCC AAT GGC AGC 1170
 Lys Thr Val Trp Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser
 270 275 280

CTT GGT GCC ATG CAT GTA TAC GAG AGC AAG TTC CGC AAC TGG TCC GAA 1218
 Leu Gly Ala Met His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu
 285 290 295 300

GGT TAC TCC GAC TTC GAC CGC GGA GCC TAT GTG ATC ACC TTC ATC CCC 1266
 Gly Tyr Ser Asp Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro
 305 310 315

30 AAG AGC TGG AAC ACC GCC CCC GAC AAG GTA AAG CAG GGC TGG CCG 1311
 Lys Ser Trp Asn Thr Ala Pro Asp Lys Val Lys Gln Gly Trp Pro
 320 325 330

TGATGTGAGC G 1322

35 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

45 Met Arg Tyr Thr Pro Glu Ala Leu Val Phe Ala Thr Met Ser Ala Val
 -75 -70 -65 -60

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Tyr Ala Pro Pro Asp Ser Cys Arg Arg Pro Ala Arg Pro Pro Pro Thr
 -55 -50 -45
 5 Met Ala Arg Gly Lys Arg Arg Ser Pro Thr Pro Lys Pro Thr Ala Ser
 -40 -35 -30
 Arg Arg Met Thr Ser Arg His Gln Arg Ala Gln Arg Ser Ala Pro Ala
 -25 -20 -15
 10 Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser Asp Asp Arg
 -10 -5 1 5
 Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro Tyr Arg
 10 15 20
 Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile Arg Lys
 25 30 35
 20 Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln Met Thr
 40 45 50
 Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val Thr Trp
 55 60 65
 25 Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala Ser Phe
 70 75 80 85
 Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro Arg Ser
 90 95 100
 30 Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu Ser Phe
 105 110 115
 Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala Ser Val Met
 120 125 130
 35 Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu Asp Asn
 135 140 145
 40 Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn Glu Asp
 150 155 160 165
 Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser Phe Lys
 170 175 180
 45 Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala Val Ile
 185 190 195
 Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser Ser Ala Asp
 200 205 210
 50
 55

Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro Gly Thr
 215 220 225
 5 Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser Pro Thr
 230 235 240 245
 Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe Gly Ala
 250 255 260
 10 Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly Asn His
 265 270 275
 Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr Glu Ser
 280 285 290
 15 Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg Gly Ala
 295 300 305
 Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro Asp Lys
 310 315 320 325
 20 Val Lys Gln Gly Trp Pro
 330

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACGAGCTCAA AGGAGTTGCA GGTTC CATG CGCTAT

36

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGGATCCAG ATCTCACATC ACGGCCAGCC CTGCTT

36

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACGAGCTCGT TGGGTTGACG ACCCCG

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACGAATTCTG CAGTTTTTCGC ACGTGAGCCA

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGCTTGGGAT TCTGATGACA GAGTCACTCC ACCAG

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTGGTGGAGT GACTCTGTCA TCAGAATCCC A

31

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTTGG AAG AGA AGA TCT CCA ACT CCA AAG CCA ACT GCT TCT AGA AGA 49
 Lys Arg Arg Ser Pro Thr Pro Lys Pro Thr Ala Ser Arg Arg
 -39 -35 -30

ATG ACT TCT AGA CAC CAA AGA GCT CAA AGA TCT GCT CCA GCT GCT TCT 97
 Met Thr Ser Arg His Gln Arg Ala Gln Arg Ser Ala Pro Ala Ala Ser
 -25 -20 -15 -10

TCT GCT GGT CCA TCT TTC AGA GCT CCA GAT TCT GAT GAC AGA GTC ACT 145
 Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser Asp Asp Arg Val Thr
 -5 1 5

CCA CCA G 152
 Pro Pro

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Lys Arg Arg Ser Pro Thr Pro Lys Pro Thr Ala Ser Arg Arg Met Thr
 -39 -35 -30 -25

Ser Arg His Gln Arg Ala Gln Arg Ser Ala Pro Ala Ala Ser Ser Ala
 -20 -15 -10

Gly Pro Ser Phe Arg Ala Pro Asp Ser Asp Asp Arg Val Thr Pro Pro
 -5 1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

CTGGTGGAGT GACTCTGTCA TCAGAATCTG GAGCTCTGAA AGATGGACCA GCAGAAGAAG      60
CAGCTGGAGC AGATCTTTGA GCTCTTTGGT GTCTAGAAGT CATTCTTCTA GAAGCAGTTG      120
GCTTTGGAGT TGGAGATCTT CTCTTCCA                                     148

```

Claims

1. A chemically synthesized or cloned DNA fragment containing a base sequence which encodes the following amino acid sequence:

```

          10          20          30          40
DSDDRVTTPA EPLDRMPDPY RPSYGRAETV VNNYIRKWQQ

          50          60          70          80
VYSHRDGRKQ QMTEEQREWL SYGCVGVTWV NSGQYPTNRL

          90         100         110         120
AFASFDEDRF KNELKNGRPR SGETRAEFEG RVAKESFDEE

          130         140         150         160
KGFQRAREVA SVMNRALENA HDESAYLDNL KKELANGNDA

          170         180         190         200
LRNEDARSPF YSALRNTPSF KERNGGNHDP SRMKAVIYSK

          210         220         230         240
HFWGQDRSS SADKRKYGDP DAFRPAPGTG LVDMSRDRNI

          250         260         270         280
PRSPSTPGEF FVNFDYGWFG AQTEADADKT VWTHGNHYHA

          290         300         310         320
PNGSLGAMHV YESKFRNWSE GYSDFDRGAY VITFIPKSWN

          330
TAPDKVKQGW P

```

(SEQ ID NO: 1).

2. The DNA fragment according to claim 1, wherein the 5' end of said base sequence is further ligated with a base sequence which encodes the following amino acid sequence:

-39 -30 -20 -10
KRRSPTPKP TASRRMTSRH QRAQRSAPAA SSAGPSFRAP

(SEQ ID NO: 5).

3. The DNA fragment according to claim 1, wherein the 5' end of said base sequence is further ligated with a base sequence which encodes the following amino acid sequence:

-75 -70 -60 -50
MRYTP EALVFATMSA VYAPPDSCRR PARPPPTMAR

-40 -30 -20 -10
GKRRSPTPKP TASRRMTSRH QRAQRSAPAA SSAGPSFRAP

(SEQ ID NO: 4).

4. The DNA fragment according to claim 1, wherein said fragment contains the following base sequence:

GAT TCT GAT GAC AGA GTC ACT CCA CCA GCT

GAA CCA TTG GAT AGA ATG CCA GAT CCA TAC

AGA CCA TCT TAC GGT AGA GCT GAA ACT GTT

GTC AAC AAC TAC ATT AGA AAG TGG CAA CAA

GTC TAC TCT CAC AGA GAT GGT AGA AAG CAA

CAA ATG ACT GAA GAA CAA AGA GAA TGG TTG

TCT TAC GGT TGT GTT GGT GTT ACT TGG GTT

AAC TCT GGT CAA TAC CCA ACT AAC AGA TTG

GCT TTC GCT TCT TTC GAT GAA GAT AGA TTC

AAG AAC GAA TTG AAG AAC GGT AGA CCA AGA

TCC GGT GAA ACT AGA GCT GAA TTC GAA GGT
AGA GTT GCT AAG GAA TCT TTC GAT GAA GAA
AAG GGT TTC CAA AGA GCT AGA GAA GTT GCT
TCT GTT ATG AAC AGA GCT CTA GAA AAC GCT
CAC GAT GAA TCT GCT TAC TTG GAT AAC TTG
AAG AAG GAA TTG GCC AAC GGT AAC GAT GCT
TTG AGA AAC GAA GAT GCT AGA TCC CCA TTC
TAC TCT GCT TTG AGA AAC ACT CCA TCT TTC
AAG GAA AGA AAC GGT GGT AAC CAC GAT CCA
TCC AGA ATG AAG GCT GTT ATT TAC TCT AAG
CAC TTC TGG TCT GGT CAA GAT AGA TCT TCT
TCT GCT GAT AAG AGA AAG TAC GGT GAT CCA
GAT GCT TTC AGA CCA GCT CCA GGT ACC GGT
TTG GTC GAC ATG TCC AGA GAT AGA AAC ATT
CCA AGA TCC CCA ACT TCT CCA GGT GAA GGT
TTC GTC AAC TTC GAT TAC GGT TGG TTC GGT
GCT CAA ACT GAA GCT GAT GCT GAT AAG ACT
GTT TGG ACC CAT GGT AAC CAC TAC CAC GCT
CCA AAC GGT TCT TTG GGT GCT ATG CAC GTC
TAC GAA TCT AAG TTC AGA AAC TGG TCT GAA
GGT TAC TCT GAT TTC GAT AGA GGT GCT TAC
GTT ATT ACT TTC ATT CCA AAG TCT TGG AAC
ACT GCT CCA GAC AAG GTC AAG CAA GGT TGG
CCA

(SEQ ID NO: 2).

5. The DNA fragment according to claim 4, wherein the 5' end of said base sequence is further ligated with the following base sequence:

AAGAGAAGATCTCCAACTCCAAAGCCAACTGCTTCTAGAAGAATGACTTCTAGACA
 CCAAAGAGCTCAAAGATCTGCTCCAGCTGCTTCTTCTGCTGGTCCATCTTTCAGAG
 CTCCA

(SEQ ID NO: 7).

6. The DNA fragment according to claim 1, wherein said fragment contains the following base sequence:

GACTCCGACGACAGGGTCACCCCTCCCGCCGAGCCGCTCGACAGGATGCCCCGACCC
 GTACCGTCCCTCGTACGGCAGGGCCGAGACGGTCGTCAACAACCTACATACGCAAGT
 GGCAGCAGGTCTACAGCCACCGCGACGGCAGGAAGCAGCAGATGACCGAGGAGCAA
 CGGGAGTGGCTGTCTACGGCTGCGTCCGTGTCACCTGGGTCAATTCGGGTCAGTA
 CCCCACGAACAGACTGGCCTTCGCGTCCTTCGACGAGGACAGGTTCAAGAACGAGC
 TGAAGAACGGCAGGCCCGGTCCGGCGAGACGCGGGCGGAGTTCGAGGGCCGCGTC
 GCGAAGGAGAGCTTTGATGAAGAGAAGGGGTTCAGCGGGCGCGTGAGGTGGCGTC
 CGTGATGAACAGGGCCCTGGAGAACGCCACGACGAGAGCGCTTACCTCGACAACC
 TCAAGAAGGAACTGGCGAACGGCAACGACGCCCTGCGCAACGAGGACGCCCCGTTCC
 CCGTTCTACTCGGCGCTGCGGAACACGCCGTCTTTAAGGAGCGGAACGGAGGCAA
 TCACGACCCGTCCAGGATGAAGGCCGTCATCTACTCGAAGCACTTCTGGAGCGGCC
 AGGACCGGTTCGAGTTCGGCCGACAAGAGGAAGTACGGCGACCCGGACGCTTTCGCG
 CCGGCCCCCGGGACCGGCCTGGTCGACATGTGAGGGACAGGAACATTCCGCGCAG
 CCCCACCAGCCCCGGTGAGGGATTTCGTCAATTTGACTACGGCTGGTTTCGGCGCCC
 AGACGGAAGCGGACGCCGACAAGACCGTCTGGACCCACGGAAATCACTATCACGCG
 CCCAATGGCAGCCTTGGTGCCATGCATGTATACGAGAGCAAGTTCCGCAACTGGTC
 CGAAGGTTACTCCGACTTCGACCGCGGAGCCTATGTGATCACCTTCATCCCCAAGA
 GCTGGAACACCGCCCCCGACAAGGTAAAGCAGGGCTGGCCG

(SEQ ID NO: 3).

7. The DNA fragment according to claim 6, wherein the 5' end of said base sequence is further ligated with the following base sequence:

ATGCGCTATACGCCGAGGCTCTCGTCTTCGCCACTATGAGTGC GGTTTATGCACC
 5 GCCGGATTCATGCCGTCGGCCGGCGAGGCCGCCGCCGA^ˆAATGGCGCGGGGGAAGA
 GACGAAGTCCTACGCCGAAACCTACCGCCTCACGGCGGATGACGTCGCGACATCAA
 CGCGCTCAACGAAGCGCTCCGGCCGCTTCGAGCGCCGGCCCGTCGTTCCGGGCCCC
 10 C

(SEQ. ID NO: 6).

- 15 8. An expression secretion vector including the DNA fragment of claims 1, 2, 3, 4, 5, 6, or 7.
9. The expression secretion vector according to claim 8, wherein said vector is contained in E.coli AJ12569 FERM BP-3558.
- 20 10. The expression secretion vector according to claim 8, wherein said vector is pNJ1053-BTG, as specified in example 5.
11. The expression secretion vector according to claim 8, wherein said vector is contained in Saccharomyces AJ14669 FERM BP-3585.
- 25 12. The expression secretion vector according to claim 8, wherein said vector is contained in Streptomyces lividans AKW-1 FERM BP-3586.
13. A transformant comprising a host transformed with the expression secretion vector according to claim 8.
- 30 14. The transformant according to claim 13, wherein said host is Escherichia coli.
15. The transformant according to claim 13, wherein said host is Streptomyces lividans.
- 35 16. The transformant according to claim 13, wherein said host is Sacchromyces cerevisiae.
17. A process for producing a protein having transglutaminase activity which comprises culturing the transformant according to claim 13 and recovering the protein produced.

Patentansprüche

- 45 1. Chemisch synthetisiertes oder kloniertes DNA-Fragment, enthaltend eine Basensequenz, die die folgende Aminosäuresequenz codiert:

10 20 30 40
 DSDDRVTTPA EPLDRMPDPY RPSYGRAETV VNNYIRKWQQ
 5 50 60 70 80
 VYSHRDGRKQ QMTEEQREWL SYGCVGVTVV NSGQYPTNRL
 90 100 110 120
 AFASFDEDRF KNELKNGRPR SGETRAEFEG RVAKESFDEE
 10 130 140 150 160
 KGFQRareva SVMNRALENA HDESAYLDNL KKELANGNDA
 170 180 190 200
 15 LRNEDARSPF YSALRNTPSF KERNGGNHDP SRMKAVIYSK
 210 220 230 240
 HFWSGQDRSS SADKRKYGDP DAFRPAPGTG LVDMSRDNI
 20 250 260 270 280
 PRSPTSPGEG FVNFDYGWFG AQTEADADKT VWITHGNHYHA
 290 300 310 320
 25 PNGSLGAMHV YESKFRNWSE GYSDFDRGAY VITFIPKSWN
 330
 TAPDKVKQGW P

(SEQ ID Nr.: 1)

2. DNA-Fragment nach Anspruch 1, worin das 5'-Ende der Basensequenz ferner mit einer Basensequenz ligiert ist, die die folgende Aminosäuresequenz codiert:

-39 -30 -20 -10
 KRRSPTPKP TASRRMTSRH QRAQRSAPAA SSAGPSFRAP

(SEQ ID Nr.: 5).

3. DNA-Fragment nach Anspruch 1, worin das 5'-Ende der Basensequenz ferner an eine Basensequenz ligiert ist, die die folgende Aminosäuresequenz codiert:

-75 -70 -60 -50
 MRYTP EALVFATMSA VYAPPDSCRR PARPPPTMAR
 -40 -30 -20 -10
 50 GKRRSPTPKP TASRRMTSRH QRAQRSAPAA SSAGPSFRAP

(SEQ ID Nr.: 4)

4. DNA-Fragment nach Anspruch 1, worin das Fragment die folgende Basensequenz enthält:

EP 0 481 504 B1

GAT TCT GAT GAC AGA GTC ACT CCA CCA GCT
GAA CCA TTG GAT AGA ATG CCA GAT CCA TAC
AGA CCA TCT TAC GGT AGA GCT GAA ACT GTT
GTC AAC AAC TAC ATT AGA AAG TGG CAA CAA
GTC TAC TCT CAC AGA GAT GGT AGA AAG CAA
CAA ATG ACT GAA GAA CAA AGA GAA TGG TTG
TCT TAC GGT TGT GTT GGT GTT ACT TGG GTT
AAC TCT GGT CAA TAC CCA ACT AAC AGA TTG
GCT TTC GCT TCT TTC GAT GAA GAT AGA TTC
AAG AAC GAA TTG AAG AAC GGT AGA CCA AGA

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TCC GGT GAA ACT AGA GCT GAA TTC GAA GGT
AGA GTT GCT AAG GAA TCT TTC GAT GAA GAA
AAG GGT TTC CAA AGA GCT AGA GAA GTT GCT
TCT GTT ATG AAC AGA GCT CTA GAA AAC GCT
CAC GAT GAA TCT GCT TAC TTG GAT AAC TTG
AAG AAG GAA TTG GCC AAC GGT AAC GAT GCT
TTG AGA AAC GAA GAT GCT AGA TCC CCA TTC
TAC TCT GCT TTG AGA AAC ACT CCA TCT TTC
AAG GAA AGA AAC GGT GGT AAC CAC GAT CCA
TCC AGA ATG AAG GCT GTT ATT TAC TCT AAG
CAC TTC TGG TCT GGT CAA GAT AGA TCT TCT
TCT GCT GAT AAG AGA AAG TAC GGT GAT CCA
GAT GCT TTC AGA CCA GCT CCA GGT ACC GGT
TTG GTC GAC ATG TCC AGA GAT AGA AAC ATT
CCA AGA TCC CCA ACT TCT CCA GGT GAA GGT
TTC GTC AAC TTC GAT TAC GGT TGG TTC GGT
GCT CAA ACT GAA GCT GAT GCT GAT AAG ACT
GTT TGG ACC CAT GGT AAC CAC TAC CAC GCT
CCA AAC GGT TCT TTG GGT GCT ATG CAC GTC
TAC GAA TCT AAG TTC AGA AAC TGG TCT GAA
GGT TAC TCT GAT TTC GAT AGA GGT GCT TAC

GTT ATT ACT TTC ATT CCA AAG TCT TGG AAC
ACT GCT CCA GAC AAG GTC AAG CAA GGT TGG
CCA

(SEQ ID Nr.: 2)

5. DNA-Fragment nach Anspruch 4, worin das 5'-Ende der Basensequenz ferner mit der folgenden Basensequenz ligiert ist:

AAGAGAAGATCTCCAACCTCCAAAGCCAACTGCTTCTAGAAGAATGACTTCTAGACA
...
CCAAAGAGCTCAAAGATCTGCTCCAGCTGCTTCTTCTGCTGGTCCATCTTTCAGAG
5 CTCCA

(SEQ ID Nr.: 7)

- 10 6. DNA-Fragment nach Anspruch 1, worin das Fragment die folgende Basensequenz enthält:

15 GACTCCGACGACAGGGTCACCCCTCCCGCCGAGCCGCTCGACAGGATGCCCGACCC
GTACCGTCCCTCGTACGGCAGGGCCGAGACGGTCGTCAACAACATACGCAAGT
GGCAGCAGGTCTACAGCCACCGCGACGGCAGGAAGCAGCAGATGACCGAGGAGCAA
20 CGGGAGTGGCTGTCTACGGCTGCGTCGGTGTACCTGGGTCAATTCGGGTCAGTA
CCCCACGAACAGACTGGCCTTCGCGTCCTTCGACGAGGACAGGTTCAGAACGAGC
TGAAGAACGGCAGGCCCCGGTCCGGCGAGACGCGGGCGGAGTTCGAGGGCCGCGTC
25 GCGAAGGAGAGCTTTGATGAAGAGAAGGGGTTCAGCGGGCGCGTGAGGTGGCGTC
CGTGATGAACAGGGCCCTGGAGAACGCCACGACGAGAGCGCTTACCTCGACAACC
TCAAGAAGGAACCTGGCGAACGGCAACGACGCCCTGCGCAACGAGGACGCCCCGTTC
30 CCGTTCTACTCGGCGCTGCGGAACACGCCGTCTTTAAGGAGCGGAACGGAGGCAA
TCACGACCCGTCCAGGATGAAGGCCGTCTACTCGAAGCACTTCTGGAGCGGCC
35 AGGACCGGTTCGAGTTCGGCCGACAAGAGGAAGTACGGCGACCCGGACGCTTTCGCG
CCGGCCCCCGGGACCGGCCTGGTCGACATGTCGAGGGACAGGAACATTCGCGCAG
40 CCCCACAGCCCCGGTGAGGGATTCGTCAATTTGACTACGGCTGGTTTCGGCGCCC
AGACGGAAGCGGACGCCGACAAGACCGTCTGGACCCACGGAAATCACTATCACGCG
45 CCCAATGGCAGCCTTGGTGCCATGCATGTATACGAGAGCAAGTTCGCAACTGGTC
CGAAGGTTACTCCGACTTCGACCGCGGAGCCTATGTGATCACCTTCATCCCCAAGA
50 GCTGGAACACCGCCCCCGACAAGGTAAAGCAGGGCTGGCCG

(SEQ ID Nr.: 3)

- 55 7. DNA-Fragment nach Anspruch 6, worin das 5'-Ende der Basensequenz ferner mit der folgenden Basensequenz
ligiert ist:

ATGCGCTATACGCCGGAGGCTCTCGTCTTCGCCACTATGAGTGCGGTTTATGCACC
 5 GCCGGATTTCATGCCGTCGGCCGGCGAGGCCGCCGCGCA⁵AAATGGCGCGGGGAAGA
 GACGAAGTCCTACGCCGAAACCTACCGCCTACGGCGGATGACGTCGCGACATCAA
 10 CGCGCTCAACGAAGCGCTCCGGCCGCTTCGAGCGCCGGCCCGTCGTTCCGGGCCCC
 C

(SEQ ID Nr.: 6)

8. Expressionsvektor, umfassend das DNA-Fragment der Ansprüche 1, 2, 3, 4, 5, 6 oder 7.
9. Expressions/Sekretionsvektor nach Anspruch 8, worin der Vektor in *E. coli* AJ12569 FERM BP-3558 enthalten ist.
10. Expressions/Sekretionsvektor nach Anspruch 8, worin der Vektor pNJ1053-BTG ist, wie in Beispiel 5 angegeben.
11. Expressions/Sekretionsvektor nach Anspruch 8, worin der Vektor in *Saccharomyces* AJ14669 FERM BP-3585 enthalten ist.
12. Expressions/Sekretionsvektor nach Anspruch 8, worin der Vektor in *Streptomyces lividans* AKW-1 FERM BP-3586 enthalten ist.
13. Transformante, enthaltend einen Wirt, der mit dem Expressions/Sekretionsvektor nach Anspruch 8 transformiert ist.
14. Transformante nach Anspruch 13, worin der Wirt *Escherichia coli* ist.
15. Transformante nach Anspruch 13, worin der Wirt *Streptomyces lividans* ist.
16. Transformante nach Anspruch 13, worin der Wirt *Saccharomyces cerevisiae* ist.
17. Verfahren zur Herstellung eines Proteins mit Transglutaminaseaktivität, welches die Kultur der Transformante nach Anspruch 13 und Gewinnen des produzierten Proteins umfasst.

Revendications

1. Fragment d'ADN synthétisé chimiquement ou cloné contenant une séquence de bases qui code pour la séquence d'acides aminés suivante :

10 20 30 40
 DSDDRVTPPA EPLDRMPDPY RPSYGRAETV VNNYIRKWQQ
 5 50 60 70 80
 VYSHRDGRKQ QMTEEQREWL SYGCVGVTWV NSGQYPTNRL
 90 100 110 120
 10 AFASFDEDRF KNELKNGRPR SGETRAEFEG RVAKESFDEE
 130 140 150 160
 KGFQRAREVA SVMNRALENA HDESAYLDNL KKELANGNDA
 170 180 190 200
 15 LRNEDARSPF YSALRNTPSF KERNGGNHDP SRMKAVIYSK
 210 220 230 240
 20 HFWSGQDRSS SADKRKYGDP DAFRPAPGTG LVDMSRDRNI
 250 260 270 280
 PRSPTSPGEG FVNFDYGWFG AQTEADADKT VWTHGNHYHA
 290 300 310 320
 25 PNGSLGAMHV YESKFRNWSE GYSDFDRGAY VITFIPKSWN
 330
 TAPDKVKQGW P
 30
 (SEQ ID NO: 1).

2. Fragment d'ADN selon la revendication 1, dans lequel l'extrémité 5' de ladite séquence de bases est de plus liée à une séquence de bases qui code pour la séquence d'acides aminés suivante :

-39 -30 -20 -10
 KRRSPTPKP TASRRMTSRH QRAQRSAPAA SSAGPSFRAP
 (SEQ ID NO: 5).

3. Fragment d'ADN selon la revendication 1, dans lequel l'extrémité 5' de ladite séquence de bases est de plus liée à une séquence de bases qui code pour la séquence d'acides aminés suivante :

-75 -70 -60 -50
 MRYTP EALVFATMSA VYAPPDSCRR PARPPPTMAR
 -40 -30 -20 -10
 GKRRSPTPKP TASRRMTSRH QRAQRSAPAA SSAGPSFRAP
 (SEQ ID NO: 4).

4. Fragment d'ADN selon la revendication 1, ledit fragment contenant la séquence de bases suivante :

EP 0 481 504 B1

GAT TCT GAT GAC AGA GTC ACT CCA CCA GCT
 GAA CCA TTG GAT AGA ATG CCA GAT CCA TAC
 AGA CCA TCT TAC GGT AGA GCT GAA ACT GTT
 GTC AAC AAC TAC ATT AGA AAG TGG CAA CAA
 GTC TAC TCT CAC AGA GAT GGT AGA AAG CAA
 CAA ATG ACT GAA GAA CAA AGA GAA TGG TTG
 TCT TAC GGT TGT GTT GGT GTT ACT TGG GTT
 AAC TCT GGT CAA TAC CCA ACT AAC AGA TTG
 GCT TTC GCT TCT TTC GAT GAA GAT AGA TTC
 AAG AAC GAA TTG AAG AAC GGT AGA CCA AGA
 TCC GGT GAA ACT AGA GCT GAA TTC GAA GGT
 AGA GTT GCT AAG GAA TCT TTC GAT GAA GAA
 AAG GGT TTC CAA AGA GCT AGA GAA GTT GCT
 TCT GTT ATG AAC AGA GCT CTA GAA AAC GCT
 CAC GAT GAA TCT GCT TAC TTG GAT AAC TTG
 AAG AAG GAA TTG GCC AAC GGT AAC GAT GCT

TTG AGA AAC GAA GAT GCT AGA TCC CCA TTC
 TAC TCT GCT TTG AGA AAC ACT CCA TCT TTC
 AAG GAA AGA AAC GGT GGT AAC CAC GAT CCA
 TCC AGA ATG AAG GCT GTT ATT TAC TCT AAG
 CAC TTC TGG TCT GGT CAA GAT AGA TCT TCT
 TCT GCT GAT AAG AGA AAG TAC GGT GAT CCA
 GAT GCT TTC AGA CCA GCT CCA GGT ACC GGT
 TTG GTC GAC ATG TCC AGA GAT AGA AAC ATT
 CCA AGA TCC CCA ACT TCT CCA GGT GAA GGT
 TTC GTC AAC TTC GAT TAC GGT TGG TTC GGT
 GCT CAA ACT GAA GCT GAT GCT GAT AAG ACT
 GTT TGG ACC CAT GGT AAC CAC TAC CAC GCT
 CCA AAC GGT TCT TTG GGT GCT ATG CAC GTC
 TAC GAA TCT AAG TTC AGA AAC TGG TCT GAA
 GGT TAC TCT GAT TTC GAT AGA GGT GCT TAC
 GTT ATT ACT TTC ATT CCA AAG TCT TGG AAC
 ACT GCT CCA GAC AAG GTC AAG CAA GGT TGG
 CCA
 (SEQ ID NO: 2).

5. Fragment d'ADN selon la revendication 4, dans lequel l'extrémité 5' de ladite séquence de bases est de plus liée à la séquence de bases suivante :

AAGAGAAGATCTCCAACTCCAAAGCCAACTGCTTCTAGAAGAATGACTTCTAGACA
 CCAAAGAGCTCAAAGATCTGCTCCAGCTGCTTCTTCTGCTGGTCCATCTTTCAGAG
 CTCCA
 (SEQ ID NO: 7).

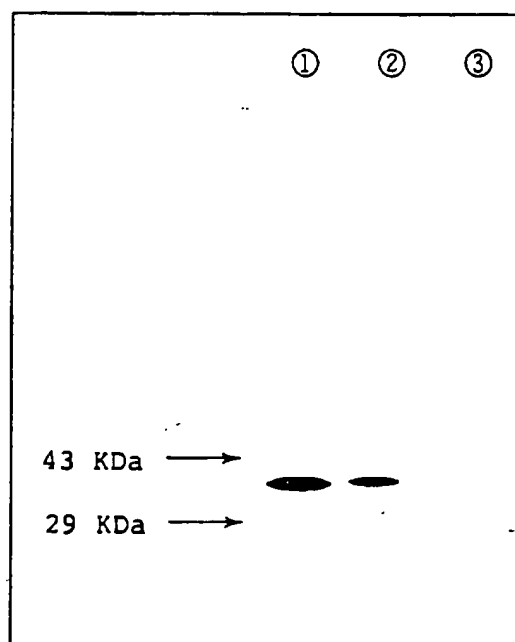
6. Fragment d'ADN selon la revendication 1, ledit fragment contenant la séquence de bases suivante :

GACTCCGACGACAGGGTCACCCCTCCCGCCGAGCCGCTCGACAGGATGCCCCGACCC
 GTACCGTCCCTCGTACGGCAGGGCCGAGACGGTCGTCAACAACACTACATACGCAAGT
 5 GGCAGCAGGTCTACAGCCACCGCGACGGCAGGAAGCAGCAGATGACCGAGGAGCAA
 CGGGAGTGGCTGTCCTACGGCTGCGTCGGTGTACCTGGGTCAATTCGGGTGAGTA
 10 CCCCACGAACAGACTGGCCTTCGCGTCCTTCGACGAGGACAGGTTCAAGAACGAGC
 TGAAGAACGGCAGGCCCGGTCCGGCGAGACGCGGGCGGAGTTCGAGGGCCGCGTC
 15 GCGAAGGAGAGCTTTGATGAAGAGAAGGGGTTCAGCGGGCGCGTGAGGTGGCGTC
 CGTGATGAACAGGGCCCTGGAGAACGCCCACGACGAGAGCGCTTACCTCGACAACC
 TCAAGAAGGAACTGGCGAACGGCAACGACGCCCTGCGCAACGAGGACGCCCCGTTCC
 20 CCGTTCTACTCGGCGCTGCGGAACACGCCGTCTTTAAGGAGCGGAACGGAGGCAA
 TCACGACCCGTCCAGGATGAAGGCCGTCATCTACTCGAAGCACTTCTGGAGCGGCC
 25 AGGACCGGTTCGAGTTCGGCCGACAAGAGGAAGTACGGCGACCCGGACGCTTTCGGC
 CCGGCCCCCGGGACCGGCCTGGTCGACATGTGAGGGACAGGAACATTCCGCGCAG
 30 CCCCACCAGCCCCGGTGAGGGATTTCGTCAATTTGACTACGGCTGGTTTCGGCGCCC
 AGACGGAAGCGGACGCCGACAAGACCGTCTGGACCCACGGAAATCACTATCACGCG
 CCCAATGGCAGCCTTGGTGCCATGCATGTATACGAGAGCAAGTCCGCAACTGGTC
 35 CGAAGGTTACTCCGACTTCGACCGCGGAGCCTATGTGATCACCTTCATCCCCAAGA
 GCTGGAACACCGCCCCCGACAAGGTAAAGCAGGGCTGGCCG
 40 (SEQ ID NO: 3).

7. Fragment d'ADN selon la revendication 6, dans lequel l'extrémité 5' de ladite séquence de bases est de plus liée à la séquence de bases suivante :

45 ATGCGCTATACGCCGAGGCTCTCGTCTTCGCCACTATGAGTGCGGTTTATGCACC
 GCCGGATTTCATGCCGTGCGCCGGCGAGGCCGCCGCGA²CAATGGCGCGGGGGAAGA
 50 GACGAAGTCCTACGCCGAAACCTACCGCCTCACGGCGGATGACGTCGCGACATCAA
 CGCGCTCAACGAAGCGCTCCGGCCGCTTCGAGCGCCGGCCCGTCGTTCCGGGCCCC
 55 C
 (SEQ ID NO: 6).

8. Vecteur d'expression-sécrétion incluant le fragment d'ADN des revendications 1, 2, 3, 4, 5, 6 ou 7.
9. Vecteur d'expression-sécrétion selon la revendication 8, ledit vecteur étant contenu dans E. coli AJ12569 FERM BP-3558.
10. Vecteur d'expression-sécrétion selon la revendication 8, ledit vecteur étant pNJ1053-BTG, comme indiqué dans l'exemple 5.
11. Vecteur d'expression-sécrétion selon la revendication 8, ledit vecteur étant contenu dans Saccharomyces AJ14669 FERM BP-3585.
12. Vecteur d'expression-sécrétion selon la revendication 8, ledit vecteur étant contenu dans Streptomyces lividans AKW-1 FERM BP-3586.
13. Transformant comprenant un hôte transformé avec le vecteur d'expression-sécrétion selon la revendication 8.
14. Transformant selon la revendication 13, dans lequel ledit hôte est Escherichia coli.
15. Transformant selon la revendication 13, dans lequel ledit hôte est Streptomyces lividans.
16. Transformant selon la revendication 13, dans lequel ledit hôte est Saccharomyces cerevisiae.
17. Procédé de production d'une protéine présentant une activité de transglutaminase, lequel comprend la culture du transformant selon la revendication 13 et la récupération de la protéine produite.



- ① Purified BTG
- ② pIJ 702-BTG
- ③ pIJ 702